



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 168511

TO: Anish Gupta  
Location: rem/3A59/3C18  
Art Unit: 1654  
Friday, May 12, 2006  
Case Serial Number: 09/759584

From: Toby Port  
Location: Biotech-Chem Library  
REM-1A59  
Phone: (571)272-2523  
[toby.port@uspto.gov](mailto:toby.port@uspto.gov)

### Search Notes

Dear Examiner Gupta,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Toby Port  
Technical Information Specialist  
STIC Biotech/Chem Library  
(571)272-2523

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# STIC SEARCH RESULTS FEEDBACK FORM

## Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact*:

Mary Hale, Information Branch Supervisor  
Remsen Bldg. 01 D86  
571-272-2507

## Voluntary Results Feedback Form

➤ I am an examiner in Workgroup:  Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature  
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC-Biotech-Chem Library, Remsen Bldg.



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STIC-Biotech/ChemLib

188511

M9

From: Gupta, Anish  
Sent: Wednesday, May 03, 2006 2:14 PM  
To: STIC-Biotech/ChemLib  
Subject: SEARCH REQUEST

Search Request:

Name: Anish Gupta  
Examiner #: 73121  
date: 5-3-06'  
Art Unit: 1654  
Phone # 2-965  
Serial Number 09/759584  
Location: 3A59  
Mailbox #: 3C18

STIC  
5-3-06  
2:14 PM

Please search the nucleic acid encoding the protein of SEQ ID NO 49, SEQ ID NO 59 and SEQ ID NO 48.

thank you

anish gupta

\*\*\*\*\*

Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

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Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

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Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIS: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 10, 2006, 04:39:06 ; Search time 2307 Seconds  
(without alignments)  
10200.775 Million cell updates/sec

Title: US-09-759-584-48  
Perfect score: 414  
Sequence: 1 GTTTATTAGTGATCGGC.....CAAAAAAAAAAAAAAAAAAAAA 414

Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_in.\*
- 3: gb\_env.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pr.\*
- 9: gb\_ro.\*
- 10: gb\_scs.\*
- 11: gb\_sy.\*
- 12: gb\_un.\*
- 13: gb\_vi.\*
- 14: gb\_htg.\*
- 15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	414	100.0	414	6	A26875 R.sativus A
2	414	100.0	414	6	A39549 Sequence 37
3	414	100.0	414	6	A63404 Sequence 19
4	414	100.0	414	6	AR050153 Sequence
5	414	100.0	414	6	ARI30272 Sequence
6	414	100.0	414	6	I23728 Sequence 48
7	414	100.0	414	6	AR207337 Sequence
8	414	100.0	414	6	AR374914 Sequence
9	414	100.0	414	6	AR642703 Sequence
10	394	95.2	395	15	RSU18557
11	255	61.6	449	6	E34290 Phage and p
12	254.2	61.4	288	6	A39553 Sequence 41
13	254.2	61.4	288	6	AR050161 Sequence
14	254.2	61.4	288	6	ARI30280 Sequence
15	254.2	61.4	288	6	I23736 Sequence 58
16	249.8	60.3	457	15	RSU18556
17	242.4	58.6	403	6	A68645 Sequence 13
18	242.4	58.6	403	15	ATANTSPEC X91916 A.thaliana

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20	232.4	56.1	575	6	BD223249
21	229	55.3	454	15	AY063779
22	223	53.9	400	6	A68647
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24	219	52.9	285	6	AR432392
25	215.8	52.1	285	6	AR014693
26	215.8	52.1	285	6	AR432393
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28	210.4	50.8	475	15	RSEFP3
29	207	50.0	499	15	RSAPF4
30	206	49.8	363	15	AF528180
31	204.8	49.5	274	15	AY133787
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33	203.4	49.1	500	6	AR432386
34	203	49.0	933	15	BOL311046
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ALIGNMENTS

RESULT 1  
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LOCUS A26875 R.sativus AFP1 gene.  
DEFINITION A26875  
ACCESSION A26875  
VERSION A26875.1 GI:1247352  
KEYWORDS  
SOURCE  
ORGANISM  
Raphanus sativus (radish)  
Raphanus sativus  
Raphanus sativus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Raphanus.  
REFERENCE  
1 (bases 1 to 414)  
AUTHORS  
Broekaert, W.F., Cammue, B.P.A., Terras, F.R.G., Vanderleyden, J., Osborn, R.W. and Rees, S.B.  
TITLE  
BIOCIDAL PROTEINS  
JOURNAL  
Patent: WO 9305153-A 33 18-MAR-1993;  
ICI PLC (GB)  
FEATURES  
Location/Qualifiers  
source  
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0;	Gaps	0;			
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RESULT 2  
A39549  
LOCUS A39549 414 bp DNA linear PAT 05-MAR-1997  
DEFINITION Sequence 37 from Patent WO9416076.  
ACCESSION A39549  
VERSION A39549.1 GI:2295942  
KEYWORDS  
SOURCE unidentified  
ORGANISM unclassified sequences.  
REFERENCE 1 (bases 1 to 414)  
AUTHORS Dubock,A.C., Powell,K.A. and Rees,S.B.  
TITLE ANTIMICROBIAL-PROTEIN-PRODUCING ENDOSYMBIOTIC MICROORGANISMS  
JOURNAL Patent: WO 9416076-A 37 21-JUL-1994;  
ZENECA LTD (GB)  
COMMENT Other publication AU 5820494 940815.  
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DEFINITION Sequence 19 from Patent WO9721814.  
ACCESSION A63404  
VERSION A63404.1 GI:3717176  
KEYWORDS  
SOURCE unidentified  
ORGANISM unclassified sequences.  
REFERENCE 1 (bases 1 to 414)  
AUTHORS Broekaert,W.F., De,S.G., Rees and Sarah,B.  
TITLE ANTIFUNGAL PROTEINS  
JOURNAL Patent: WO 9721814-A 19 19-JUN-1997;  
ZENECA LTD (GB)  
COMMENT Other publication AU 1105397 19970703.  
FEATURES  
Location/Qualifiers  
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ORIGIN  
Query Match 100.0%; Score 414; DB 6; Length 414;  
Best Local Similarity 100.0%; Pred. No. 1.4e-82;  
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 361 GTTGGTTCGGTTATACAAATAAGTTTATTCACCAAAAAAATAAAAAA 414  
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RESULT 4  
AR050153  
LOCUS AR050153 414 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 48 from patent US 5824869.  
ACCESSION AR050153  
VERSION AR050153.1 GI:5972145  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 414)  
AUTHORS Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,  
Terras,F.R.G. and Vanderleyden,J.  
TITLE Biotidal proteins  
JOURNAL Patent: US 5824869-A 48 20-OCT-1998;  
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Best Local Similarity 100.0%; Pred. No. 1.4e-82;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
LOCUS      AR130272      414 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 48 from patent US 6187904.
ACCESSION  AR130272
VERSION     AR130272.1 GI:14118169
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 414)
AUTHORS   Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,
          Terras,F.R.G. and Vanderleyden,J.
TITLE     Biocidal proteins
JOURNAL   Patent: US 6187904-A 48 13-FEB-2001;
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RESULT 6
LOCUS      I23728      414 bp      DNA      linear      PAT 07-OCT-1996
DEFINITION Sequence 48 from patent US 5538525.
ACCESSION  I23728
VERSION     I23728.1 GI:1603598
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 414)
AUTHORS   Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,
          Terras,F.R.G. and Vanderleyden,J.
TITLE     Biocidal proteins
JOURNAL   Patent: US 5538525-A 48 23-JUL-1996;
FEATURES   Location/Qualifiers
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Query Match      100.0%; Score 414; DB 6; Length 414;
Best Local Similarity 100.0%; Pred. No. 1.4e-82;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GTTCTTTTGGCTGCTTTTGAAGCACCACCAACAATGGTGGGAAGCACAGAAGTTGGCGAAAG 120
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Db 61 GTTCTTTTGGCTGCTTTTGAAGCACCACCAACAATGGTGGGAAGCACAGAAGTTGGCGAAAG 120

QY 121 CCAAGTGGGACATGGTCAGAGTCTGTGGAACAATAACGCATGCAAGAAATCAGTGCATT 180
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QY 361 GTTGGTTCGGTTATACAAATAAAGTTTATTACCAAAAAAATAAAAAA 414
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AR207337
LOCUS AR207337 414 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 19 from patent US 6372888.
ACCESSION AR207337
VERSION AR207337.1 GI:21506219
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS De Samblanx,G.Wivina., Broekaert,W.Frans. and Rees,S.Bronwen.
TITLE Antifungal proteins
JOURNAL Patent: US 6372888-A 19 16-APR-2002;
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source Location/Qualifiers
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Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LOCUS AR642703 414 bp DNA linear PAT 20-APR-2005
DEFINITION Sequence 19 from patent US 6864068.
ACCESSION AR642703
VERSION AR642703.1 GI:62779939
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Rees,S.B., De Samblanx,G.W. and Broekaert,W.F.
TITLE Antifungal proteins
JOURNAL Patent: US 6864068-A 19 08-MAR-2005;
Syngenta Limited; Guilford;
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Best Local Similarity 100.0%; Pred. No. 1.4e-82;
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LOCUS AR374914 414 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 45 from patent US 6605698.
ACCESSION AR374914
VERSION AR374914.1 GI:40077932
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Van Amerongen,A., Pant,F., Borremans,F.A., De Samblanx,G.W., Sijtsma,L., Meeloen,R.H., Fuijk,W.C., Schaaper,W.M.M., Broekaert,W.F., van Gelder,W.M.J. and Rees,S.B.
TITLE Antifungal peptides and composition thereof
JOURNAL Patent: US 6605698-A 45 12-AUG-2003;
Syngenta Limited; Guilford;
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QY 61 GTTCTTTTGGTCTCTTTCGAAGCACCACCAATGGTGGGAAGCACAAGTTGTGCGAAAG 120
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RESULT 9
LOCUS AR642703 414 bp DNA linear PAT 20-APR-2005
DEFINITION Sequence 19 from patent US 6864068.
ACCESSION AR642703
VERSION AR642703.1 GI:62779939
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Rees,S.B., De Samblanx,G.W. and Broekaert,W.F.
TITLE Antifungal proteins
JOURNAL Patent: US 6864068-A 19 08-MAR-2005;
Syngenta Limited; Guilford;
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Best Local Similarity 100.0%; Pred. No. 1.4e-82;
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Db  89  GTTTTCTGCTTTGGAAGCACCACCAATAGTGGTGAAGCAGCAAGTTGTGTCAGAGGCCA 148

QY  124  AGTGGGACATGGTCAGGAGTCTGTGGAACAATAACGCATGCAAGAATCAGTGCATTAAAC 183
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Db  149  AGTGGGACATGGTCAGGAGTCTGTGGAATAATAACGCATGCAAGAATCAGTGCATTGCA 208

QY  184  CTTGAGAAAGCAGCATGGATCTTGCAACTATGTCTTCCAGCTCACAAAGTGATCTGC 243
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QY  244  TACTTCTCTGTTAAAT-TATCGCAAACTCTTTGGTGAATAGT--TTATGTAATTTAC 300
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QY  301  ACAAAATACTCAGTGTCACTATCCATGATGATTTTAAGACATGACCAGATATG-TTA 359
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Db  329  AATTAATAAGTTGTGTCACTATTATTAGTGACTTTATGACATGTGCCAGGTATGTTTA 388

QY  360  TGTGTGTTGGTTATACAAATAAAGTTTATTACCAAAATAAAAAAAAA 410
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Db  389  TGTGTGTTGGTTGTAATATAAAAAGTTTACGGATATAATAAGATGATAA 439

RESULT 12
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LOCUS      A39553      288 bp      DNA      linear      PAT 05-MAR-1997
DEFINITION Sequence 41 from Patent WO9416076.
ACCESSION A39553
VERSION   A39553.1  GI:2295844
KEYWORDS .
SOURCE    unidentified
          unclassified sequences.
REFERENCE 1 (bases 1 to 288)
AUTHORS  Dubock,A.C., Powell,K.A. and Rees,S.B.
TITLE    ANTIMICROBIAL-PROTEIN-PRODUCING ENDOSYMBIOTIC MICROORGANISMS
JOURNAL  Patent: WO 9416076-A 41 21-JUL-1994;
        ZENECA LTD (GB)
COMMENT  Other publication AU 5820494 940815.
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ACCESSION A130280
VERSION   A130280.1  GI:14118177
KEYWORDS .
SOURCE    Unknown.
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REFERENCE 1 (bases 1 to 288)
AUTHORS  Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,

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ACCESSION A050161
VERSION   A050161.1  GI:5972153
KEYWORDS .
SOURCE    Unknown.
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REFERENCE 1 (bases 1 to 288)
AUTHORS  Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,
        Terras,F.R.G. and Vanderleyden,J.
TITLE    Bioicidal proteins
JOURNAL  Patent: US 5824869-A 58 20-OCT-1998;
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VERSION   A130280.1  GI:14118177
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SOURCE    Unknown.
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REFERENCE 1 (bases 1 to 288)
AUTHORS  Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,
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Terras,F.R.G. and Vanderleyden,J.  
Biocidal proteins  
JOURNAL  
Patent: US 6187904-A 58 13-FEB-2001;  
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ACCESSION 123736  
VERSION 123736.1 GI:1603606  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 288)  
AUTHORS Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,  
Terras,F.R.G. and Vanderleyden,J.  
TITLE Biocidal proteins  
JOURNAL Patent: US 5538525-A 58 23-JUL-1996;  
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4	414	100.0	414	2	AAT68696		AAT68696 Radish an
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25	196.6	47.5	243	6	ADG87651		Adg87651 A. thalia
26	196.6	47.5	243	6	ADG87824		Adg87824 A. thalia
27	196.6	47.5	243	8	ABZ42136		Abz42136 Arabidops
28	194.6	47.0	308	2	AAT94577		Aat94577 Cloned 5'
29	193.8	46.8	481	2	AAT99289		Aat99289 Alyseum s
30	180	43.5	270	2	AAT94582		Aat94582 Amplified
31	178.8	43.2	286	2	AAT94574		Aat94574 Alyseum s
32	178	43.0	1973	3	AAC46924		Aac46924 Arabidops
33	156.8	37.9	522	3	AAZ99324		Aaz99324 DNA encod
34	154.2	37.2	534	3	AAZ99327		Aaz99327 DNA encod
35	153.6	37.1	606	3	AAZ99326		Aaz99326 DNA encod
36	153.6	37.1	1616	2	AAV10646		Aav10646 A. thalia
37	152.4	36.8	534	3	AAZ51396		Aaz51396 Portion o
38	152.4	36.8	534	3	AAZ99325		Aaz99325 DNA encod
39	151.4	36.6	485	3	AAZ99333		Aaz99333 DNA encod
40	147.6	35.7	443	3	AAZ99330		Aaz99330 DNA encod
41	145.8	35.2	485	3	AAZ99337		Aaz99337 DNA encod
42	145.8	35.2	1093	3	AAZ99334		Aaz99334 DNA encod
43	145.4	35.1	437	3	AAZ99331		Aaz99331 DNA encod
44	145	35.0	434	3	AAZ99332		Aaz99332 DNA encod
45	144.6	34.9	488	3	AAZ99338		Aaz99338 DNA encod

## ALIGNMENTS

## RESULT 1

AAQ38650  
ID AAQ38650 standard; DNA; 414 BP.

XX AC AAQ38650;

XX DT 25-MAR-2003 (revised)  
DT 07-JUL-1993 (first entry)

XX DE Rs-APPI CDNA.

XX KW Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria;  
KW fungicide; bactericide; antibiotic; antifungal; gram positive;  
KW plant disease resistance; low toxicity.

XX OS Raphanus sativus.

XX FH Key Location/Qualifiers  
XX CDS 16..256  
XX FT /\*tag= a

XX PN WO9305153-A1.

XX PD 18-MAR-1993.

XX PF 27-AUG-1992; 92WO-GB001570.

XX PR 29-AUG-1991; 91GB-00018523.

XX PR 13-FEB-1992; 92GB-00003038.

XX PR 25-JUN-1992; 92GB-00013526.

XX PA (ICIL ) IMPERIAL CHEM IND PLC.

XX PI Broekaert WF, Cammue BPA, Osborn RW, Rees SB, Terras PRG;

XX PI Vanderleyden J;

XX DR WPI; 1993-100978/12.

XX PT Biotidal proteins isolated from seeds of plants - e.g. brassica or  
PT dahlia, useful for increasing plants' resistance to fungal and bacterial  
XX diseases.

PS Example 21; Fig 35; 110pp; English.

XX This cDNA represents the sequence of Rs-AFP1 from *Raphanus sativus*. PCR

CC primer AAQ38640 was used together with AAQ38641 to generate a probe for

CC screening a *Raphanus sativus* seed cDNA library. This primer corresponds

CC to amino acids 2 to 7 of Rs-AFP1 and has a sense orientation. The 144bp

CC product was partially re-amplified using AAQ38642 and AAQ38641 to give a

CC 123bp product, which was further reamplified with the same primers and

CC digoxigenin-11-dUTP instead of dTTP to give a digoxigenin labeled PCR

CC product. This was used to screen a lambda ZAPII cDNA library by in situ

CC plaque hybridisation. Positive plaques were purified and subjected to two

CC additional screening rounds with the same probe. Inserts were excised in

CC vivo into the pBluescript phagemid form with the aid of helper phage

CC R408. Inserts from 22 positive clones were excised by EcoRI digestion and

CC their size compared by agarose gel electrophoresis. Four clones had

CC insert sizes of approx. 400bp the others between 250-300bp. The inserts

CC of the 4 largest clones were then sequenced and found to differ only in

CC the length of their 5' and 3' UTR's. The longest sequence is given here.

CC (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;

Query Match 100.0%; Score 414; DB 2; Length 414;

Best Local Similarity 100.0%; Pred. No. 6e-92;

Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTATTAGTATCATGGCTAAGTTTGGTCCATCATCGCACTCTTTTGGTCTCTT 60

DB 1 GTTTATTAGTATCATGGCTAAGTTTGGTCCATCATCGCACTCTTTTGGTCTCTT 60

QY 61 GTTCTTTTGGTCTCTTTCGAAGCACCACCAATGGTGAAGCAGCAAGTTGTGCGAAGG 120

DB 61 GTTCTTTTGGTCTCTTTCGAAGCACCACCAATGGTGAAGCAGCAAGTTGTGCGAAGG 120

QY 121 CCAAGTGGGACATGGTTCAGAGTCTGTGGAACAATAACGATGCAAGAAATCAGTGCATT 180

DB 121 CCAAGTGGGACATGGTTCAGAGTCTGTGGAACAATAACGATGCAAGAAATCAGTGCATT 180

QY 181 AACCTTGGGACATGGTTCAGAGTCTGTGGAACAATAACGATGCAAGAAATCAGTGCATT 240

DB 181 AACCTTGGGACATGGTTCAGAGTCTGTGGAACAATAACGATGCAAGAAATCAGTGCATT 240

QY 241 TGTACTTTCTTGTGTTAATTTATCGCAAACTCTTTGGTGAATAGTTTATGTAATTAC 300

DB 241 TGTACTTTCTTGTGTTAATTTATCGCAAACTCTTTGGTGAATAGTTTATGTAATTAC 300

QY 301 ACAAATAAGTCAAGTCTCACTATCCATGATGATTTTAAAGACATGTACCAGATATGTTAT 360

DB 301 ACAAATAAGTCAAGTCTCACTATCCATGATGATTTTAAAGACATGTACCAGATATGTTAT 360

QY 361 GTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAAAAAAAAAAAAAAAAA 414

DB 361 GTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAAAAAAAAAAAAAAAAA 414

RESULT 2

AAQ70128

ID AAQ70128 standard; cDNA; 414 BP.

XX AAQ70128;

AC AAQ70128;

DT 25-MAR-2003 (revised)

DT 14-FEB-1995 (first entry)

XX Antimicrobial Rs-AFP1.

XX Antimicrobial; Rs-AFP1; symbiosis; disease-resistance; fungus-resistance;

KW Clavibacter xyl. subsp. cynodontis; Cxc; crop improvement; endophyte; ss.

XX *Raphanus sativus*.

OS WO9416076-A1.

XX

PD 21-JUL-1994.

XX

PF 05-JAN-1994; 94WO-GB0000012.

XX

PR 08-JAN-1993; 93GB-000000281.

XX (ZENE ) ZENECA LTD.

PA

XX Dubock AC, Powell KA, Rees SB;

PI

XX WPI; 1994-249223/30.

DR P-PSDB; AAR57325.

XX Antimicrobial protein producing endo-symbiotic microorganisms - is

PT produced by combining nucleic acids encoding the protein with an

PT endophyte, useful for protecting plant hosts from esp. fungal disease.

XX

PS Disclosure; Page 31; 39pp; English.

XX

CC Plant-derived antimicrobial proteins are expressed in endosymbiotic

CC Clavibacter xyl. subsp. cynodontis (Cxc). Plants or seeds treated with

CC recombinant Cxc are protected against fungal disease. A suitable

CC antimicrobial protein is Rs-AFP1 from *R. sativus*. The full-length cDNA

CC sequence of Rs-AFP1 is given in AAQ70128. (Updated on 25-MAR-2003 to

CC correct PN field.)

XX SQ Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;

Query Match 100.0%; Score 414; DB 2; Length 414;

Best Local Similarity 100.0%; Pred. No. 6e-92;

Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTATTAGTATCATGGCTAAGTTTGGTCCATCATCGCACTCTTTTGGTCTCTT 60

DB 1 GTTTATTAGTATCATGGCTAAGTTTGGTCCATCATCGCACTCTTTTGGTCTCTT 60

QY 61 GTTCTTTTGGTCTCTTTCGAAGCACCACCAATGGTGAAGCAGCAAGTTGTGCGAAGG 120

DB 61 GTTCTTTTGGTCTCTTTCGAAGCACCACCAATGGTGAAGCAGCAAGTTGTGCGAAGG 120

QY 121 CCAAGTGGGACATGGTTCAGAGTCTGTGGAACAATAACGATGCAAGAAATCAGTGCATT 180

DB 121 CCAAGTGGGACATGGTTCAGAGTCTGTGGAACAATAACGATGCAAGAAATCAGTGCATT 180

QY 181 AACCTTGGGACATGGTTCAGAGTCTGTGGAACAATAACGATGCAAGAAATCAGTGCATT 240

DB 181 AACCTTGGGACATGGTTCAGAGTCTGTGGAACAATAACGATGCAAGAAATCAGTGCATT 240

QY 241 TGTACTTTCTTGTGTTAATTTATCGCAAACTCTTTGGTGAATAGTTTATGTAATTAC 300

DB 241 TGTACTTTCTTGTGTTAATTTATCGCAAACTCTTTGGTGAATAGTTTATGTAATTAC 300

QY 301 ACAAATAAGTCAAGTCTCACTATCCATGATGATTTTAAAGACATGTACCAGATATGTTAT 360

DB 301 ACAAATAAGTCAAGTCTCACTATCCATGATGATTTTAAAGACATGTACCAGATATGTTAT 360

QY 361 GTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAAAAAAAAAAAAAAAAA 414

DB 361 GTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAAAAAAAAAAAAAAAAA 414

RESULT 3

AA72333

ID AA72333 standard; cDNA; 414 BP.

XX AA72333;

AC AA72333;

DT 25-MAR-2003 (revised)

DT 19-JAN-1998 (first entry)

XX *Raphanus sativus* antifungal protein I (Rs-AFP1) cDNA.

DE Antifungal protein; candida; fungal resistance; food additive; radish;

XX

KW

```
crop protection; plant defensin; bacterial protection; preservative; ss.
Raphanus sativus.
Key Location/Qualifiers
CDS 16..258
FT /tag= a
FT /transl_except= (pos:85..87, aa:Glu)
FT sig_peptide 16..102
FT /tag= b
FT mat_peptide 103..255
FT /tag= c
FT /product= "antifungal_protein_1"
XX WO9721815-A2.
XX
XX
XX 19-JUN-1997.
XX
XX 12-DEC-1996; 96WO-GB003068.
XX
XX 13-DEC-1995; 95GB-00025455.
XX 28-MAR-1996; 96GB-00006552.
XX (ZENE ) ZENECA LTD.
XX
XX Melloen RH, Puijk WC, Schaaper WMM, Sijtsma L, Van Amerongen A;
PI Broekaert W, Samblanx GW, Fant F, Borremans FAM, Rees SB;
PI Van Gelder WMJ;
XX
XX WPI; 1997-332786/30.
XX P-PSDB; AAW19280.
XX
XX Antifungal peptide derived from radish antifungal protein 2 - and related
XX DNA, useful for producing plants with increased fungal resistance and as
XX therapeutic or preservative agent.
XX Claim 8; Fig 2; 65pp; English.
XX
XX This cDNA sequence encodes an Raphanus sativus (radish) antifungal
XX protein (Rs-APP1). Analogues of the homologous protein, Rs-APP2
XX (AAW19281), have also been produced (see AAW19282-92, AAW19294-98,
XX AAW19301-04, AAW19330-34 and AAW31765-834). Plants containing DNA
XX sequences encoding these proteins have improved resistance to fungi.
XX Compositions containing the peptides can be used to control fungi or
XX bacteria in pharmaceutical (e.g. treatment of Candida infections) or
XX preservative purposes (as food additives). In agriculture, the peptide
XX may be used to improve disease resistance or disease tolerance of crops,
XX either pre or post harvest. When applied to plants they may also have
XX curative as well as protective actions. The peptides may also be used to
XX protect plants by introducing them, or a microorganism capable of
XX expressing the peptide into the soil. (Updated on 25-MAR-2003 to correct
XX PI field.)
XX
XX Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
Query Match 100.0%; Score 414; DB 2; Length 414;
Best Local Similarity 100.0%; Pred. No. 6e-92;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTTATTAGTATCATGCTAAGTTTGGTCCATCATCGCACTTCTTTTGTCTCTT 60
DB |||||||
DB 1 GTTTATTAGTATCATGCTAAGTTTGGTCCATCATCGCACTTCTTTTGTCTCTT 60
QY 61 GTTCTTTTGTCTCTTCCAAACCAACAAGTGGGAAGCACAGAGTTGGCCAAAGG 120
DB |||||||
DB 61 GTTCTTTTGTCTCTTCCAAACCAACAAGTGGGAAGCACAGAGTTGGCCAAAGG 120
QY 121 CCAAGTGGACATGCTCAGAGTCTGTGGAACAATAACGATGCAAGTCAAGTCAATT 180
DB |||||||
DB 121 CCAAGTGGACATGCTCAGAGTCTGTGGAACAATAACGATGCAAGTCAAGTCAATT 180
QY 181 AACCTTGAGAAAGCAGCATCGATCTTGCACATATGTTTCCCAAGCTCACAAGTGTATC 240
DB |||||||
Db 181 AACCTTGAGAAAGCAGCATCGATCTTGCACATATGTTTCCCAAGCTCACAAGTGTATC 240
QY 241 TGCTACTTTCTCTTGTAAATTTTATCGCAAACTCTTTGGTGAATAGTTTATGTAATTTAC 300
DB |||||||
Db 241 TGCTACTTTCTCTTGTAAATTTTATCGCAAACTCTTTGGTGAATAGTTTATGTAATTTAC 300
QY 301 ACAAATAAGTCAGTGTCTCACTATCATGAGTGATTTTAAAGACATGTACCAGATATGTTAT 360
DB |||||||
Db 301 ACAAATAAGTCAGTGTCTCACTATCATGAGTGATTTTAAAGACATGTACCAGATATGTTAT 360
QY 361 GTTGTTCGGTTATACAAATAAAGTTTATTTCACCAAAAAA 414
DB |||||||
Db 361 GTTGTTCGGTTATACAAATAAAGTTTATTTCACCAAAAAA 414
RESULT 4
AAT68696
ID AAT68696 standard; cDNA; 414 BP.
XX
XX AAT68696;
XX
XX 13-DEC-1997 (first entry)
XX
XX DE Radish antifungal protein 1 (Rs-APP1) cDNA.
XX
XX Rs-APP1; radish antifungal protein 1; fungicide; salt tolerance;
XX KW preservative; transgenic plant; crop protection.
XX OS Raphanus sativus.
XX
XX FH Key Location/Qualifiers
XX CDS 16..258
XX FT /tag= a
XX FT /transl_except= (pos:85..87, aa:Glu)
XX FT sig_peptide 16..102
XX FT /tag= b
XX FT mat_peptide 103..255
XX FT /tag= c
XX
XX WO9721814-A1.
XX
XX PN 19-JUN-1997.
XX
XX PD 12-DEC-1996; 96WO-GB003065.
XX
XX PF 13-DEC-1995; 95GB-00025474.
XX
XX PR (ZENE ) ZENECA LTD.
XX
XX PA Broekaert WF, De Samblanx GW, Rees SB;
XX PI WPI; 1997-332785/30.
XX
XX DR P-PSDB; AAW19617.
XX
XX PT New active mutants of radish antifungal protein 2 - used to generate
XX fungus-resistant plants or as therapeutic or preservative agents.
XX
XX PS Disclosure; Fig 2; 39pp; English.
XX
XX CC This cDNA clone codes for the preprotein for radish antifungal protein 1
XX (Rs-APP1) (AAW19617). Novel antifungal proteins are based on Rs-APP1, Rs-
XX APP2 (see AAW19616), Rs-APP3 and Rs-APP4, especially those in which Gly9
XX is replaced by Arg, Val39 by Arg, Gly9 by Arg, Glu5 by Met and/or Gly16 by
XX Met. Mutants (see AAW26371-90) of Rs-APP2 are specifically claimed. The
XX mutants show improved salt tolerant antifungal activity, particularly
XX when expressed in plants
XX
XX SQ Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
Query Match 100.0%; Score 414; DB 2; Length 414;
Best Local Similarity 100.0%; Pred. No. 6e-92;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 GTTTTATTAGTCATGCTGAAGTTTGGTCCATCGCACTTCTTTTGGCTGCTTT 60  
 |||||  
 Db 1 GTTTTATTAGTCATGCTGAAGTTTGGTCCATCGCACTTCTTTTGGCTGCTTT 60  
 |||||  
 QY 61 GTTCTTTTGGCTGCTTTGGAAGCACCACCAATGTTGGTGAAGCAGAGAGTTGTGCGAAAGG 120  
 |||||  
 Db 61 GTTCTTTTGGCTGCTTTGGAAGCACCACCAATGTTGGTGAAGCAGAGAGTTGTGCGAAAGG 120  
 |||||  
 QY 121 CCAAGTGGACATGTCAGAGTCTGTGGAACAATAACGCATGCAAGATCAGTGCATT 180  
 |||||  
 Db 121 CCAAGTGGACATGTCAGAGTCTGTGGAACAATAACGCATGCAAGATCAGTGCATT 180  
 |||||  
 QY 181 AACCTTGAGAAAGCAGACATGATCTGCAACTATGCTTCCAGCTCACAAGTGTATC 240  
 |||||  
 Db 181 AACCTTGAGAAAGCAGACATGATCTGCAACTATGCTTCCAGCTCACAAGTGTATC 240  
 |||||  
 QY 241 TGTACTTTTCTTTGTTAAATTTATCGCAAACTCTTTTGGTGAATAGTTTATGTAATTTAC 300  
 |||||  
 Db 241 TGTACTTTTCTTTGTTAAATTTATCGCAAACTCTTTTGGTGAATAGTTTATGTAATTTAC 300  
 |||||  
 QY 301 ACAAATAAGTCAGTGTCTACTATCCATGAGTGAATTTTAAGACATGTACAGATATGTTAT 360  
 |||||  
 Db 301 ACAAATAAGTCAGTGTCTACTATCCATGAGTGAATTTTAAGACATGTACAGATATGTTAT 360  
 |||||  
 QY 361 GTTGGTTCGGTTATACAAATAAAGTTTATTACCAAAAAA 414  
 |||||  
 Db 361 GTTGGTTCGGTTATACAAATAAAGTTTATTACCAAAAAA 414  
 |||||

## RESULT 5

ADCS1221  
 ID ADCS1221 standard; DNA; 394 BP.

XX AC ADCS1221;

XX DT 18-DEC-2003 (first entry)

XX DE Brassica oleracea defensin protein coding sequence.

XX KW antimicrobial protein; defensin; transgenic plant;  
 KW composite disease resistance; pathogenic bacteria;  
 KW rice white leaf blight; brown-stripe disease; glume blight;  
 KW seedling damping-off disease; filamentous fungi; rice blight;  
 KW sheath blight disease; leaf blight; gene; ds.

XX OS Brassica oleracea.

XX FH Key Location/Qualifiers

XX FT CDS 1..243

XX FT /\*tag= a

XX FT /product= "Brassica oleracea defensin protein"

XX JP2003088379-A.

XX PN 25-MAR-2003.

XX PF 18-SEP-2001; 2001JP-00283117.

XX PR 18-SEP-2001; 2001JP-00283117.

XX PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.

XX WPI; 2003-621123/59.

XX DR P-PSDB; ADCS1222.

XX PT Novel protein from Brassica campestris, useful as antimicrobial against  
 PT plant pathogenic filamentous fungi or pathogenic bacteria, especially for  
 PT treating e.g. rice white leaf blight and sheath blight disease.

XX PS Claim 3; SEQ ID NO 1; 34pp; Japanese.

XX SS The invention comprises the amino acid and coding sequences of  
 CC antimicrobial (defensin) proteins from Brassica. The DNA and protein

CC sequences of the invention are useful for producing transformed plants  
 CC with composite disease resistance, especially resistant to diseases  
 CC caused by pathogenic bacteria, such as: rice white leaf blight, brown-  
 CC stripe disease, glume blight, and seedling damping-off disease. As well  
 CC as diseases caused by filamentous fungi, such as: rice blight, sheath  
 CC blight disease, and leaf blight. The present DNA sequence encodes a  
 CC Brassica defensin protein of the invention.

SQ Sequence 394 BP; 116 A; 71 C; 82 G; 125 T; 0 U; 0 Other;

Query Match 78.2%; Score 323.8; DB 10; Length 394;

Best Local Similarity 90.4%; Pred. No. 8.8e-70;

Matches 357; Conservative 0; Mismatches 37; Indels 1; Gaps 1;

QY 16 ATGGCTAAGTTTGGCTCCATCATCGCACTTCTTTTGGTCTGCTTTTGGCTGCT 75  
 |||||

Db 1 ATGGCTAAGTTTGGTCCATCATCGCCCTACTTTTGGTCTGCTTTTGGCTGCT 60  
 |||||

QY 76 TTCTGAAGCACCACCAATGTTGGGAAGCAGCAAGATTTGTGCAAGGCCAAGTGGACATGG 135  
 |||||

Db 61 CTCGAAGCACCACCAATGTTGGGAAGCAGCAAGATTTGTGCGAGGCCAAGTGGACATGG 120  
 |||||

QY 136 TCAGGAGTCTGTGGAACAATAACGCATGCAAGAATCAGTGCATTAACTTGAGAAAGCA 195  
 |||||

Db 121 TCAGGAGTCTGTGGAACAATAACGCATGCAAGAATCAGTGCATTAACTTGAGAAAGCA 180  
 |||||

QY 196 CGACATGGATCTTGCACATGATGCTTCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255  
 |||||

Db 181 CGACATGGATCTTGCACATGATGCTTCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 240  
 |||||

QY 256 TAAATTTATCGCAAACTCTTTTGGTGAATAGTTTATGTAATTTTACAAAAAATAGTCAGT 315  
 |||||

Db 241 TAACTTTATCGCAAACTCTTTTGGTGAATAGTTTATGTAATTTTACAAAAAATAGTCAGT 300  
 |||||

QY 316 GTCACATATCCATGAGTGAATTTAAGACATGTACCGAGATGATGTTGCTGGTTATA 375  
 |||||

Db 301 GTCACATATCAATGAGTGAATTTATGACATGTACCTGATATGTTATGTTGGTTATA 360  
 |||||

QY 376 CAATATAAGTTTATTCACCAAAAAA 410  
 |||||

Db 361 -ATATAAAGTTTATTCACCAAAAAA 394  
 |||||

## RESULT 6

ADU71300

ID ADU71300 standard; cDNA; 394 BP.

XX AC ADU71300;

XX DT 10-FEB-2005 (first entry)

XX DE Brassica oleracea defensin protein coding sequence - SEQ ID 1.

XX KW antimicrobial; plant disease resistance; gene; ss; defensin.

XX OS Brassica oleracea.

XX FH Key Location/Qualifiers

XX FT CDS 1..243

XX FT /\*tag= a

XX FT /product= "Brassica oleracea defensin protein - SEQ ID 2"

XX PN JP2004329215-A.

XX WPI; 2004-809169/80.

XX PD 25-NOV-2004.

XX PF 07-JUN-2004; 2004JP-00168986.

XX PR 18-SEP-2001; 2001JP-00283117.

XX PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.

XX WPI; 2004-809169/80.

```
DR P-PSDB; ADU71301.
XX
PT Novel Brassica sp. derived protein having antimicrobial activity, useful
PT for producing multiple disease resistant plants.
XX
PS Example 2; SEQ ID NO 1; 16pp; Japanese.
XX
CC The invention comprises the amino acid and coding sequence of an
CC antimicrobial protein obtained from Brassica sp. The DNA and protein
CC sequences of the invention are useful in the production of a multiple
CC disease resistant plant. The present cDNA sequence encodes the Brassica
CC oleracea defensin protein.
XX
SQ Sequence 394 BP; 116 A; 71 C; 82 G; 125 T; 0 U; 0 Other;
XX
Query Match 78.2%; Score 323.8; DB 13; Length 394;
Best Local Similarity 90.4%; Pred. No. 8.8e-70;
Matches 357; Conservative 0; Mismatches 37; Indels 1; Gaps 1;
QY 16 ATGGCTAAGTTTGGTCCATCATCGCACTCTTTTGGCTGCTCTTTTGGCTGCT 75
Db 1 ATGGCTAAGTTTGGTCCATCATCGCACTCTTTTGGCTGCTCTTTTGGCTGCT 60
QY 76 TTCGAAGCACCACAAATGCTGAAGCAGAGAAGTTGTGCAAGGCCCAAGTGGACATGG 135
Db 61 CTCGAAGCACCACAAATGCTGAAGCAGAGAAGTTGTGCGAGAGGCCCAAGTGGACATGG 120
QY 136 TCAGAGTCTGTGGAACAATAACGCATCGCAAGATCAGTGCATTAACCTTCGAGAAAGCA 195
Db 121 TCAGAGTCTGTGGAACAATAACGCATCGCAAGATCAGTGCATTAACCTTCGAGAAAGCA 180
QY 196 CGACATGATCTTGGCAATATGCTCTTCCAGCTCACAAGTATCTGTCTACTTCTTCTGT 255
Db 181 CGACATGATCTTGGCAATATGCTCTTCCAGCTCACAAGTATCTGTCTACTTCTTCTGT 240
QY 256 TAAATTTATCGCAAACTCTTGGTGAATAGTATTTATGTAATTAATTAAGTCAAGT 315
Db 241 TAACTTATGCGCAAACTCTTGGTGAATAGTATTTATGTAATTAATTAAGTCAAGT 300
QY 316 GTCACTATCCATGAGTGAATTTAAGACATGATGATGATGATGATGATGATGATGATGAT 375
Db 301 GTCACTATCCATGAGTGAATTTAAGACATGATGATGATGATGATGATGATGATGATGAT 360
QY 376 CAAATAAAGTTTATTCACCAAAAAA 410
Db 361 -ATATAAGTTTATTCACCAAAAAA 394
RESULT 7
ID ADC51223
XX ADC51223 standard; DNA; 426 BP.
XX
AC ADC51223;
XX
DT 18-DEC-2003 (first entry)
XX
DE Brassica defensin protein coding sequence.
XX
KW antimicrobial protein; defensin; transgenic plant;
KW composite disease resistance; pathogenic bacteria;
KW rice white leaf blight; brown-stripe disease; glume blight;
KW seedling damping-off disease; filamentous fungi; rice blight;
KW sheath blight disease; leaf blight; gene; ds.
XX
OS Brassica sp.
XX
FH Key Location/Qualifiers
FT CDS 1..243
FT /tag= a
FT /product= "Brassica defensin protein"
XX
PN JP2003088379-A.
XX
```

```
PD 25-MAR-2003.
XX
XX 18-SEP-2001; 2001JP-00283117.
XX
XX 18-SEP-2001; 2001JP-00283117.
XX
PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
XX
XX WPI; 2003-621123/59.
XX
XX P-PSDB; ADC51224.
XX
PT Novel protein from Brassica campestris, useful as antimicrobial against
PT plant pathogenic filamentous fungi or pathogenic bacteria, especially for
PT treating e.g. rice white leaf blight and sheath blight disease.
XX
XX Claim 3; SEQ ID NO 3; 34pp; Japanese.
XX
XX The invention comprises the amino acid and coding sequences of
XX antimicrobial (defensin) proteins from Brassica. The DNA and protein
XX sequences of the invention are useful for producing transformed plants
XX with composite disease resistance, especially resistant to diseases
XX caused by pathogenic bacteria, such as: rice white leaf blight, brown-
XX stripe disease, glume blight, and seedling damping-off disease. As well
XX as diseases caused by filamentous fungi, such as: rice blight, sheath
XX blight disease, and leaf blight. The present DNA sequence encodes a
XX Brassica defensin protein of the invention.
XX
SQ Sequence 426 BP; 142 A; 72 C; 84 G; 128 T; 0 U; 0 Other;
XX
Query Match 74.3%; Score 307.8; DB 10; Length 426;
Best Local Similarity 88.8%; Pred. No. 7.6e-66;
Matches 356; Conservative 0; Mismatches 42; Indels 3; Gaps 2;
QY 16 ATGGCTAAGTTTGGTCCATCATCGCACTCTTTTGGCTGCTCTTTTGGCTGCT 75
Db 1 ATGGCTAAGTTTGGTCCATCATCGCACTCTTTTGGCTGCTCTTTTGGCTGCT 60
QY 76 TTCGAAGCACCACAAATGCTGAAGCAGAGAAGTTGTGCAAGGCCCAAGTGGACATGG 135
Db 61 TTCGAAGCACCACAAATGCTGAAGCAGAGAAGTTGTGCGAGAGGCCCAAGTGGACATGG 120
QY 136 TCAGAGTCTGTGGAACAATAACGCATCGCAAGATCAGTGCATTAACCTTCGAGAAAGCA 195
Db 121 TCAGAGTCTGTGGAACAATAACGCATCGCAAGATCAGTGCATTAACCTTCGAGAAAGCA 180
QY 196 CGACATGATCTTGGCAATATGCTCTTCCAGCTCACAAGTATCTGTCTACTTCTTCTGT 255
Db 181 CGACATGATCTTGGCAATATGCTCTTCCAGCTCACAAGTATCTGTCTACTTCTTCTGT 240
QY 256 TAAATTTATCGCAAACTCTTGGTGAATAGTATTTATGTAATTAATTAAGTCAAGT 315
Db 241 TAACTTATGCGCAAACTCTTGGTGAATAGTATTTATGTAATTAATTAAGTCAAGT 300
QY 316 GTCACTATCCATGAGTGAATTTAAGACATGATGATGATGATGATGATGATGATGATGAT 373
Db 301 GTCACTATCCATGAGTGAATTTAAGACATGATGATGATGATGATGATGATGATGATGAT 360
QY 374 TACAATAAAGTTTATTCACCAAAAAA 414
Db 361 TA-ATAAAGTTTATTCACCAAAAAA 400
RESULT 8
ADU71302
ID ADU71302 standard; DNA; 426 BP.
XX
XX AC ADU71302;
XX
XX DT 10-FEB-2005 (first entry)
XX
XX DE Brassica antimicrobial protein coding sequence - SEQ ID 3.
XX
XX KW antimicrobial; plant disease resistance; gene; ds.
```

```

XX OS Brassica sp.
XX FH Key Location/Qualifiers
XX CDS 1..243
FT /tag= a
FT /product= "Brassica antimicrobial protein - SEQ ID 4"
XX
XX JP2004329215-A.
XX
XX PD 25-NOV-2004.
XX
XX PF 07-JUN-2004; 2004JP-00168986.
XX
XX PR 18-SEP-2001; 2001JP-00283117.
XX
XX PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGOU SEIBUTSU SH.
XX
XX DR WPI; 2004-809169/80.
XX
XX DR P-PSDB; ADU71303.
XX
XX PT Novel Brassica sp. derived protein having antimicrobial activity, useful
XX for producing multiple disease resistant plants.
XX
XX PS Claim 3; SEQ ID NO 3; 16pp; Japanese.
XX
XX CC The invention comprises the amino acid and coding sequence of an
XX antimicrobial protein obtained from Brassica sp. The DNA and protein
XX sequences of the invention are useful in the production of a multiple
XX disease resistant plant. The present DNA sequence encodes the Brassica
XX antimicrobial protein of the invention.
XX
XX SQ Sequence 426 BP; 142 A; 72 C; 84 G; 128 T; 0 U; 0 Other;

Query Match 74.3%; Score 307.8; DB 13; Length 426;
Best Local Similarity 88.8%; Pred. No. 7.6e-66;
Matches 356; Conservative 0; Mismatches 42; Indels 3; Gaps 2;

QY 16 ATGGCTAAGTTGGTGCATCATCGCACTCTTTTGGCTGCTGTTCTTTTGGTCT 75
DB 1 ATGGCCAAAGTTTGTGCTATCATTTGCCCACTTTTGGCTGCTTGTCTTTTAGCTGCT 60

QY 76 TTGGAAGCACCACAAATGTGGAAGCAGCAAGAGTTGTGGAAGGCGCAAGTGGGACATGG 135
DB 61 TTGAGGACACCAACATGTGTGAGAGCAGAGAGTTGTGGAAGGCGCAAGTGGGACATGG 120

QY 136 TCAGGAGTCTGTGGAACCAATAACCGCATCAAGAAATCAGTGCATTAACTTGAGAAAGCA 195
DB 121 TCAGGAGTCTGTGGAACCAATAACCGCATCAAGAAATCAGTGCATTAACTTGAGAAAGCA 180

QY 196 CGACATGGATCTTGGAACTATGCTTCCAGCTCACAAGTGATCTGCTACTTCTCTTGT 255
DB 181 CGACATGGATCTTGGAACTATGCTTCCAGCTCACAAGTGATCTGCTACTTCTCTTGT 240

QY 256 TAATTTATCGCAACTCTTTGGTGAATAGTTTATGTAATTTACACAAATAAGTCACT 315
DB 241 TAATTTATCGGCAACTCTTTGGTGAATAGTTTATGTAATTTACACAAATAAGTCACT 300

QY 316 GTCACATATCCATGAGTGAATTTTAAGACATGTACC--AGATATGTTATGTTGGTTCGGTTA 373
DB 301 GTCACATATCAATGAGTGAATTTATGACATGTACCTCATATATGTTATGTTGGTTCGGTTA 360

QY 374 TACAAATAAGTTTATTCACCAAAAAAAAAAAAAAAAAAAAA 414
DB 361 TA-ATAAAAAGTTTATGACCCGTTCAAAAAAAAAAAAAAAAAAAAA 400

RESULT 9
AA53190
ID AA53190 standard; DNA; 449 BP.
XX
XX AC AA53190;
XX

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DT 06-OCT-2000 (first entry)
XX
XX Raphanus sativus antibacterial protein radishin encoding DNA SEQ ID NO:1.
XX
XX Raphanus sativus; antibacterial; plant; resistance; paddy; radishin;
XX pathogenic microbe; radish; rice blast disease; ds.
XX
XX OS Raphanus sativus.
XX
XX FN JP2000116379-A.
XX
XX PD 25-APR-2000.
XX
XX PF 09-OCT-1998; 98JP-00288472.
XX
XX PR 09-OCT-1998; 98JP-00288472.
XX
XX PA (TOYA-) TOYAMA KEN.
XX
XX DR WPI; 2000-389821/34.
XX
XX DR P-PSDB; AAY91117.
XX
XX PT Isolated DNA from Raphanus sativus used to transform a microbe and a
XX plant to produce an antibacterial protein used to increase resistance of
XX rice paddy against pathogenic microbes.
XX
XX PS Claim 1; Page 4; 7pp; Japanese.
XX
XX CC The present sequence encodes an antibacterial protein, designated
XX radishin, isolated from Raphanus sativus (radish). A phage or plasmid
XX comprising radishin can be used for increasing resistance of paddy and
XX rice blast disease against pathogenic microbes
XX
XX SQ Sequence 449 BP; 126 A; 78 C; 94 G; 151 T; 0 U; 0 Other;

Query Match 61.6%; Score 255; DB 3; Length 449;
Best Local Similarity 81.0%; Pred. No. 7.4e-53;
Matches 333; Conservative 0; Mismatches 74; Indels 4; Gaps 3;

QY 4 TTATTAGTATCATGGCTAAGTTTGGTCCCATCATCGCACTTCTTTTGGCTGCTTGT 63
DB 29 TTAGTAGTATCATGGCTAAGTTTGGTCCCATCATCGCACTTCTTTTGGCTGCTTGT 88

QY 64 CTTTGTGCTGCTTTCGAAGCACCACAAATGGTGAAGCAGACAGAAAGTTGCGAAAGGCCA 123
DB 89 GTTTTGTGCTTTCGAAGCACCACAAATGGTGAAGCAGACAGAAAGTTGTCAGAGGCCA 148

QY 124 AGTGGACATGGTTCAGGAGTCTGTGGAACCAATAACGCATGCAAGAAATCAGTGCATTAA 183
DB 149 AGTGGACATGGTTCAGGAGTCTGTGGAACCAATAACGCATGCAAGAAATCAGTGCATTAA 208

QY 184 CTTGGAAGACGACATGGATCTTGCACATATGCTTCCAGCTCACAAGTGTATCTGC 243
DB 209 CTTGGAAGACGACATGGGTTTGCACATATGCTTCCAGCTCACAAGTGTATCTGT 268

QY 244 TACTTTCTCTGTTAAT--TATCGCAAACTCTTTGGTGAATAGTTT--TTATGTAATTTAC 300
DB 269 TATTTCCCTTGTAAATTCATTAACCTCTCGGTGGTTAATAGTGGCGCATTTTACATAT 328

QY 301 ACAAAATAGTCAGTGTCTACTATCCATGATGATGATTTTAAAGACATGTPACAGATATG-TTA 359
DB 329 AATTAATAGTTTGTGTCATATTATTATTAGTCACTTTATGACATGTGCGCAGGTATCTGTTA 388

QY 360 TGTGTGTTGGTTATACAAATAAGTTTATTACCACCAAAAAAAAAAAAAA 410
DB 389 TGTGTGTTGGTTATATAAAAAAGTTTACCGATATAAATAGATGATAA 439

RESULT 10
AAQ38652
ID AAQ38652 standard; DNA; 261 BP.
XX
XX AC AAQ38652;
XX

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XX 25-MAR-2003 (revised)
DT 07-JUL-1993 (first entry)
XX
DB Rs-APP2 cDNA.
XX
KW Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria;
KW fungicide; bacteriocide; antibiotic; antifungal; gram positive;
KW plant disease resistance; low toxicity.
XX
OS Raphanus sativus.
XX
FH Key Location/Qualifiers
FT CDS 16..256
FT /tag= a
XX
XX WO9305153-A1.
XX
XX 18-MAR-1993.
XX
XX 27-AUG-1992; 92WO-GB001570.
XX
XX 29-AUG-1991; 91GB-00018523.
XX
XX 13-FEB-1992; 92GB-00003038.
XX
XX 25-JUN-1992; 92GB-00013526.
XX
XX (ICIL ) IMPERIAL CHEM IND PLC.
XX
XX Broekaert WF, Cammue BPA, Osborn RW, Rees SB, Terras FRG;
XX Vanderleyden J;
XX
XX WPI; 1993-100978/12.
XX
XX Biocidal proteins isolated from seeds of plants - e.g. brassica or
XX dahlia, useful for increasing plants' resistance to fungal and bacterial
XX diseases.
XX
XX Example 21; Fig 35; 110pp; English.
XX
XX This cDNA represents the sequence of Rs-APP2 from Raphanus sativus. PCR
XX primer AAQ38640 was used together with AAQ38641 to generate a probe for
XX screening a Raphanus sativus seed cDNA library. This primer corresponds
XX to amino acids 2 to 7 of Rs-APP1 and has a sense orientation. The 144bp
XX product was partially re-amplified using AAQ38642 and AAQ38641 to give a
XX 123bp product, which was further reamplified with the same primers and
XX digoxigenin-11-dUTP instead of dTTP to give a digoxigenin labeled PCR
XX product. This was used to screen a lambda ZAPII cDNA library by in situ
XX plaque hybridisation. Positive plaques were purified and subjected to two
XX additional screening rounds with the same probe. Inserts were excised in
XX vivo into the pBluescript phagemid form with the aid of helper phage
XX R408. Inserts from 22 positive clones were excised by EcoRI digestion and
XX their size compared by agarose gel electrophoresis. Four clones had
XX insert sizes of approx. 400bp the others between 250-300bp. The inserts
XX of the 4 largest clones were then sequenced and found to differ only in
XX the length of their 5' and 3' UTR's. The longest sequence was identified
XX as Rs-APP1 (AAQ38650). Rs-APP2 was seen to differ by only 2 amino acids
XX from Rs-APP1, so the Rs-APP1 cDNA was transformed to the Rs-APP2
XX nucleotide sequence by PCR assisted site directed mutagenesis. (Updated
XX on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 261 BP; 67 A; 55 C; 59 G; 80 T; 0 U; 0 Other;

Query Match 61.4%; Score 254.2; DB 2; Length 261;
Best Local Similarity 98.8%; Pred. No. 1e-52;
Matches 256; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTTATTAGTATCATGGCTAAGTTTGGTCCATCATCGCACTTCTTTTGTGCTCTT 60
DB 1 GTTTATTAGTATCATGGCTAAGTTTGGTCCATCATCGCACTTCTTTTGTGCTCTT 60

QY 61 GTTCTTTTGTGCTTTTGAAGCACCACCAATGGTGGAGCAGACAGAGTTGTGCAAGG 120
DB 61 GTTCTTTTGTGCTTTTGAAGCACCACCAATGGTGGAGCAGACAGAGTTGTGCAAGG 120

QY 121 CCAAGTGGGACATGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 180
DB 121 CCAAGTGGGACATGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 180

QY 181 AACCTTGAAGAACGACGACATGGATCTTGGCAACTATGTCTTCCAGCTCACAGTGTATC 240
DB 181 AGACTTGAAGAACGACGACATGGATCTTGGCAACTATGTCTTCCAGCTCACAGTGTATC 240

QY 241 TGCTACTTTCTCTTGTAAAT 259
DB 241 TGCTACTTTCTCTTGTAAAT 259

RESULT 11
AAQ70130
ID AAQ70130 standard; cDNA; 288 BP.
XX
XX AC AAQ70130;
XX
XX 25-MAR-2003 (revised)
XX 14-FEB-1995 (first entry)
XX
XX DE Antimicrobial Rs-APP2.
XX
XX KW Antimicrobial; Rs-APP2; symbiosis; disease-resistance; fungus-resistance;
XX Clavibacter xyli subsp. cynodontis; Cxc; crop improvement; endophyte;
XX PCR; polymerase chain reaction; mutagenesis; ss.
XX
XX OS Raphanus sativus.
XX
XX WO9416076-A1.
XX
XX 21-JUL-1994.
XX
XX 05-JAN-1994; 94WO-GB0000012.
XX
XX 08-JAN-1993; 93GB-00000281.
XX
XX (ZENE ) ZENECA LTD.
XX
XX Dubock AC, Powell KA, Rees SB;
XX
XX WPI; 1994-249223/30.
XX
XX P-PSDB; AAR57327.
XX
XX Antimicrobial protein producing endo-symbiotic microorganisms - is
XX produced by combining nucleic acids encoding the protein with an
XX endophyte, useful for protecting plant hosts from esp. fungal disease.
XX
XX Disclosure; Page 33; 39pp; English.
XX
XX Plant-derived antimicrobial proteins are expressed in endosymbiotic
XX Clavibacter xyli subsp. cynodontis (Cxc). Plants or seeds treated with
XX recombinant Cxc are protected against fungal disease. A suitable
XX antimicrobial protein is Rs-APP1 from R. sativus. The full-length cDNA
XX sequence of PCR assisted site-directed mutagenesis of Rs-APP2 is given in
XX AAQ70130 and the deduced amino acid sequence in AAR57327. (Updated on 25-
XX MAR-2003 to correct PN field.)
XX
SQ Sequence 288 BP; 70 A; 66 C; 69 G; 83 T; 0 U; 0 Other;

Query Match 61.4%; Score 254.2; DB 2; Length 288;
Best Local Similarity 98.8%; Pred. No. 1e-52;
Matches 256; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTTATTAGTATCATGGCTAAGTTTGGTCCATCATCGCACTTCTTTTGTGCTCTT 60
DB 28 GTTTATTAGTATCATGGCTAAGTTTGGTCCATCATCGCACTTCTTTTGTGCTCTT 87

QY 61 GTTCTTTTGTGCTTTTGAAGCACCACCAATGGTGGAGCAGACAGAGTTGTGCAAGG 120
DB 88 GTTCTTTTGTGCTTTTGAAGCACCACCAATGGTGGAGCAGACAGAGTTGTGCAAGG 147

```



CC The present sequence encodes a protein of the invention, comprising the  
 CC mature proteins of the plant defensins, the Dahlia antimicrobial protein  
 CC (AMP) 1 and the antifungal protein 2 (RsAFP2), linked by a linker  
 CC propeptide of the invention. The specification describes methods for  
 CC improving expression levels of one or more proteins in a transgenic  
 CC plant. The method comprises inserting a DNA sequence having a promoter  
 CC region operably linked to two or more protein encoding regions separated  
 CC by a DNA sequence coding for a linker propeptide and a terminator region.  
 CC The method is used to produce proteins in plants. The linker propeptide  
 CC comprising a cleavage site, whereby the expressed polypeptide is post-  
 CC translationally processed into the component protein molecules. The  
 CC propeptide sequence is rich in amino acids A, V, S and T and contains  
 CC dipeptidic sequences consisting of either two acidic, two basic or one  
 CC acidic and one basic residue as a cleavable linker sequence  
 XX  
 XX Sequence 575 BP; 133 A; 137 C; 149 G; 156 T; 0 U; 0 Other;

Query Match 56.1%; Score 232.4; DB 3; Length 575;  
 Best Local Similarity 95.6%; Pred. No. 2.8e-47;  
 Matches 239; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
 QY 10 GTGATCATGGCTAAGTTGGTCCATCATCGCACTTCTTTTGGCTGCTCTTGTCTTTT 69  
 Db 318 GGGCCCATGGCTAAGTTGGTCCATCATCGCACTTCTTTTGGCTGCTCTTGTCTTTT 377  
 QY 70 GCTGCTTTTCCAGCACCAACAATGGTGGAGCAGACAGAGTTGTGCGAAGGCCAAGTGGG 129  
 Db 378 GCTGCTTTTCCAGCACCAACAATGGTGGAGCAGACAGAGTTGTGCGAAGGCCAAGTGGG 437  
 QY 130 ACATGCTCAGGAGTCTGTGGAACAATACGATGCAAGTCAAGTCAAGTCAAGTCAAGT 189  
 Db 438 ACATGCTCAGGAGTCTGTGGAACAATACGATGCAAGTCAAGTCAAGTCAAGTCAAGT 497  
 QY 190 AAGACGACGATGATGCTTGGCAACTATGCTTCCAGCTCACAAGTGTATCTGCTACTTT 249  
 Db 498 AAGACGACGATGATGCTTGGCAACTATGCTTCCAGCTCACAAGTGTATCTGCTACTTT 557  
 QY 250 CCTTGTGAAT 259  
 Db 558 CCTTGTGAAT 567

RESULT 14  
 AAV10633  
 ID AAV10633 standard; DNA; 400 BP.

XX AAV10633;

XX 23-JUN-1998 (first entry)

XX A. thaliana PDF1.2 DNA.

XX Defensin; PDF1.2; protection; plant; pathogen; jasmonate; ethylene;  
 XX fungi; ss.

XX Arabidopsis thaliana.

XX Key Location/Qualifiers  
 XX CDS 32..274

XX sig\_peptide /\*tag= a

XX mat\_peptide /\*tag= b

XX /\*tag= c

XX /product= "PDF1.2"

XX /note= "Plant defensin"

XX WO9800023-A2.

XX 08-JAN-1998.

XX 20-JUN-1997; 97WO-GB001672.

PR 01-JUL-1996; 96GB-00013753.

XX (ZENE ) ZENECA LTD.

XX Broekaert WF, Thomma BPHJ, Penninckx IAMA, Terras FRG, Manners JM;  
 XX Kazan K;

XX WPI; 1998-086663/08.

XX P-PSDB; AAW40346.

XX Protecting plants against pathogens by inducing defensin genes - by  
 XX stimulating ethylene or jasmonate pathways, also new promoter of defensin  
 XX gene from Arabidopsis.

XX Disclosure; Fig 1; 72pp; English.

XX This sequence encodes the Arabidopsis PDF1.2 gene which is used in a  
 XX novel method for the protection of plants against pathogens which  
 XX involves inducing expression of a plant defensin gene by stimulating the  
 XX jasmonate and/or ethylene pathways. The method is used to induce  
 XX protection against necrotrophic pathogens, specifically fungi and does  
 XX not require cytotoxic or potentially harmful chemicals  
 XX  
 XX Sequence 400 BP; 109 A; 82 C; 80 G; 125 T; 0 U; 4 Other;

Query Match 53.9%; Score 223; DB 2; Length 400;  
 Best Local Similarity 79.9%; Pred. No. 5.2e-45;  
 Matches 274; Conservative 0; Mismatches 67; Indels 2; Gaps 1;

QY 5 TATTAGTATCATGCTAAGTTTGGTCCATCATCGCACTTCTTTTGGCTGCTCTTGTTC 64  
 Db 21 TAATAATCATCATGCTAAGTTTGGTCCATCATCGCACTTCTTTTGGCTGCTCTTGTTC 80

QY 65 TTTTGTGCTTTTCCAGCACCAACAATGGTGGAGCAGACAGAGTTGTGCGAAGGCCAA 124  
 Db 81 TCTTTGTGCTTTTCCAGCACCGGCAATGGTGGAGCAGACAGAGTTGTGCGAAGGCCAA 140

QY 125 GTGGGACATGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGTCAAGTCAAGTCAAGT 184  
 Db 141 GTGGGACATGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGTCAAGTCAAGTCAAGT 200

QY 185 TTGAGAAAGCAGACATGATCTTGCACATATGCTTCCAGCTCACAAGTGTATCTGCT 244  
 Db 201 TTGAGAGGAGCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 260

QY 245 ACTTTCTTGTGTTAATTTATCGCAACTCTTTGCGAATAGTTTATGTAATTTACACAA 304  
 Db 261 ACGTCCCATGTTAATTTATCGCAACTCTTTGCGAATAGTTTATGTAATTTATGTAATTT 320

QY 305 AATAAGTCAGTGTCTACTATCCATGATGATGATGATGATGATGATGATGATGATGATGAT 347  
 Db 321 AATAAGTCAGTGTCTACTATCCATGATGATGATGATGATGATGATGATGATGATGATGAT 361

RESULT 15

ID ADZ75091 standard; DNA; 400 BP.

XX AC ADZ75091;

XX 30-JUN-2005 (first entry)

XX Arabidopsis leaf-specific open reading frame, SEQ ID 607.

XX Crop improvement; gene; ds; plant; plant disease; plant fungal disease;  
 XX drought resistance; herbicide resistance; insect resistance;  
 XX abiotic stress tolerance; salt tolerance; heat tolerance; cold tolerance;  
 XX gene expression; food.

XX Arabidopsis thaliana.

XX WO200198480-A2.

XX

PD 27-DEC-2001.  
XX  
PF 22-JUN-2001; 2001WO-IB001104.  
XX  
PR 23-JUN-2000; 2000US-0213848P.  
PR 23-JUN-2000; 2000US-0214087P.  
PR 29-DEC-2000; 2000US-0258692P.  
XX  
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX  
XX Budworth P, Brown D, Chang H, Zhu T, Han B, Wang X, Cooper B;  
XX WPI; 2002-055861/07.  
XX  
XX Promoters for root-specific, leaf-specific or constitutive regulation of  
PT plant gene expression, useful for regulating the expression of selected  
PT transgenes (e.g. stress tolerance and defence related genes) in  
PT economically important plants.  
XX  
PS Disclosure; SEQ ID NO 607; 290pp; English.  
XX  
XX The invention relates to promoters for root-specific, leaf-specific or  
CC constitutive regulation of plant gene expression. Also included are an  
CC isolated polynucleotide (N1) (comprising a plant nucleotide sequence that  
CC directs root-specific transcription of an operatively linked nucleic acid  
CC segment in a plant cell, where the plant nucleotide sequence is from a  
CC gene encoding a polypeptide that is substantially similar to a  
CC polypeptide encoded by an Arabidopsis gene comprising a promoter selected  
CC from AD274492-AD274543, AD275008-AD275016 or AD275036-AD275034 or a  
CC polypeptide encoded by a Rice gene comprising a promoter selected from  
CC AD275309 and AD275327, an isolated polynucleotide (N2) (comprising a plant  
CC nucleotide sequence that directs constitutive transcription of an  
CC operatively linked nucleic acid segment in a plant cell, where the plant  
CC nucleotide sequence is from a gene encoding a polypeptide that is  
CC substantially similar to a polypeptide encoded by an Arabidopsis gene  
CC comprising a promoter selected from AD274543-AD274830, AD274968-AD275006,  
CC AD275007, AD275035-AD275069, AD275310-AD275326 and AD275328-AD275359), an  
CC isolated polynucleotide (N3) (comprising a plant nucleotide sequence that  
CC directs leaf-specific transcription of an operatively linked nucleic acid  
CC segment in a plant, where the plant nucleotide sequence is from a gene  
CC encoding a polypeptide that is substantially similar to a polypeptide  
CC encoded by an Arabidopsis gene having a promoter selected from one of  
CC AD275177-AD275257, a recombinant vector comprising N1-N3, an expression  
CC cassette comprising N1-N3 operatively linked to an open reading frame, a  
CC recombinant vector comprising the above expression cassette, a host cell  
CC comprising the expression cassette, a plant cell containing the  
CC expression cassette, a transformed plant (the genome of which is  
CC augmented with the expression cassette), a transformed plant comprising  
CC transformed plant cells (where the cells contain the expression  
CC cassette), a method (M1) for augmenting a plant genome, a method (M2) to  
CC identify a gene having a promoter (the expression of which is altered in  
CC root), a method (M3) to identify a gene having a promoter (the expression  
CC of which is constitutive in a plant cell), a method (M4) to identify a  
CC gene having a promoter (the expression of which is altered in leaves of a  
CC plant), and a method to alter the phenotype of a plant cell comprising  
CC introducing the expression cassette, for the expression cassette, the  
CC open reading frame is from an insect resistance gene, a bacterial disease  
CC resistance gene, a fungal disease resistance gene, a viral disease  
CC resistance gene, a nematode disease resistance gene, a herbicide  
CC resistance gene, a stress resistance gene, a gene affecting grain  
CC composition or quality, a nutrient utilization gene, a mycotoxin  
CC reduction gene, a male sterility gene, a selectable marker gene, a  
CC screenable marker gene, a negative selectable marker, a gene affecting  
CC plant agronomic characteristics, or an environment or stress resistance  
CC gene. The stress resistance gene confers resistance or tolerance to  
CC drought, heat, chilling, freezing, excessive moisture, excessive salt, or  
CC excessive oxidative stress. The promoters are useful for regulating the  
CC expression of selected transgenes in economically important plants. For  
CC example, root-specific promoters may be useful for expressing defense-  
CC related genes, including those conferring insecticidal resistance and  
CC stress tolerance genes, e.g., salt, cold or drought tolerance, and genes  
CC for altering nutrient uptake, and leaf-specific promoters may be useful  
CC for producing large quantities of protein, for expressing oils or

CC proteins of interest, and genes for increasing the nutritional value of a  
CC plant. Constitutive promoters are useful for expressing a wide variety of  
CC genes including those which alter metabolic pathways, confer disease  
CC resistance, for protein production, e.g., antibody production, or to  
CC improve nutrient uptake. The present sequence is an open reading frame  
CC from an Arabidopsis leaf specific promoter gene of the invention. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX

SQ Sequence 400 BP; 109 A; 82 C; 80 G; 125 T; 0 U; 4 Other;

Query Match	53.9%;	Score 223;	DB 7;	Length 400;
Best Local Similarity	79.9%;	Pred. No. 5.2e-45;		
Matches 274;	Conservative	0;	Mismatches 67;	Indels 2;
Gaps	1;			

  

QY	5	TATTAGTGAATCAGGCTAAGTTGGTCCATCATGCGCACTTCTTTTGGTCTCTTGTTC	64
DB	21	TAATAATCATCATGCTAAGTTGGTTCATCATCACCCCTTATCTTCGGTCTCTTGTTC	80
QY	65	TTTTTGTCTGCTTTCGAAGCACCAACAATGCTGAGACACAGAAAGTTGCGAAAGCCAA	124
DB	81	TCTTTGCTCTTTCGACGCCCGCAATGCTGAGACACAGAAAGTTGCGAGAGCCAA	140
QY	125	GTGGGACATGTCAGGAGTCTGTGGAACAATAAGCATGCAAGATCAGTGCATTAAAC	184
DB	141	GTGGGACATGTCAGGAGTCTGTGGAACAATAAGCATGCAAGATCAGTGCATTAAAC	200
QY	185	TTGAGAAACACGACGATGATCTTGCAACTATGCTTCCAGCTCAAGTGTATCTGCT	244
DB	201	TTGAAGGAGCCAAACATGATCATGCAACTATGCTTCCAGCAGCACAAGTGTATCTGT	260
QY	245	ACTTTCTTGTAAATTTATGCGCAAACTCTTGGTGAATAGTTTATGTAATTTACACA	304
DB	261	ACGTCCCATGTTAAATCTTACCACTAATCTTGGTGCTAAATCGTGTATTTTACATAA	320
QY	305	AATAAGTCAGTGTCACTATCCATGAGTGAATTTTAAAGACATGTA	347
DB	321	AATAAGTCAGTGTCACTATCCATGAGTGAATTTTAAAGACATGTA	361

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Maximum Match 100%  
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4: gb\_est4:  
5: gb\_est5:  
6: gb\_est6:  
7: gb\_est7:  
8: gb\_est8:  
9: gb\_est9:  
10: gb\_est10:  
11: gb\_est11:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
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2	326.8	78.9	547	7	CN726625 3ETMS UP
3	326.6	78.7	566	7	CN725823 3ETMS UP
4	324.4	78.4	484	7	CN726272 3ETMS UP
5	324.4	78.4	485	7	CN726374 3ETMS UP
6	322.8	78.0	481	7	CN726255 3ETMS UP
7	320.7	77.3	456	7	CN726661 3ETMS UP
8	316.4	76.4	458	7	CN726701 3ETMS UP
9	315.6	76.2	597	7	CN726329 3ETMS UP
10	315.2	76.1	453	7	CN726424 3ETMS UP
11	313.8	75.8	413	7	CN826227 EL1386 Br
12	313.8	75.8	458	6	CD834994 BN45.0430
13	311.2	75.2	470	6	CD831680 BN40.060H
14	311.1	75.1	446	6	CD834088 BN45.040H
15	311.1	75.1	452	6	CD832071 BN40.0610
16	310.6	75.0	519	6	CD835064 BN45.044C
17	310.7	74.9	447	6	CD832592 BN40.0630
18	309.4	74.7	408	6	CD833779 BN45.001I
19	309.4	74.7	409	6	CD834090 BN45.040I
20	309.4	74.7	450	6	CD834611 BN45.042H
21	308.6	74.5	438	6	CD831294 BN40.058H
22	307	74.2	420	6	CD833944 BN45.040B

23	307	74.2	421	6	CD826491	CD826491	BN25.064A
24	307	74.2	422	6	CD833983	CD833983	BN45.040D
25	307	74.2	426	6	CD827413	CD827413	BN25.067G
26	307	74.2	438	6	CD831479	CD831479	BN40.059J
27	307	74.2	553	6	CD831014	CD831014	BN40.047K
28	305.4	73.8	418	6	CD832825	CD832825	BN40.064A
29	305.4	73.8	419	6	CD834168	CD834168	BN45.040N
30	305.4	73.8	421	6	CD833977	CD833977	BN45.040D
31	305.4	73.8	421	6	CD837517	CD837517	BN45.052I
32	303.8	73.4	453	6	CD834008	CD834008	BN45.040E
33	303.2	73.2	592	7	CN726094	CN726094	17ACDHMS
34	302.2	73.0	421	6	CD831111	CD831111	BN40.058A
35	302.2	73.0	422	6	CD831972	CD831972	BN40.061I
36	302.2	73.0	424	6	CD833048	CD833048	BN40.065M
37	302.2	73.0	480	6	CD828332	CD828332	BN25.070H
38	277.6	67.1	373	7	CN726757	CN726757	3ETMS UP
39	276	66.7	458	7	CN827136	CN827136	EL2049R B
40	275.2	66.5	449	6	CD833047	CD833047	BN40.065M
41	268.2	64.8	425	6	CD834852	CD834852	BN45.043G
42	268.2	64.8	523	6	CD833661	CD833661	BN45.001C
43	268.2	64.8	543	6	CD828840	CD828840	BN40.040A
44	268	64.7	473	6	CD834995	CD834995	BN45.0430
45	266.6	64.4	427	6	CD833613	CD833613	BN40.067P

ALIGNMENTS

RESULT 1  
CN726241  
LOCUS  
DEFINITION 3ETMS UP\_001\_G04\_10JUN2003\_010 Brassica napus 3ETMS Brassica napus linear EST 14-MAY-2005  
CDNA 5', mRNA sequence.  
ACCESSION CN726241  
VERSION CN726241.1 GI:55284043  
KEYWORDS EST.  
SOURCE Brassica napus (rape)  
ORGANISM Brassica napus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
REFERENCE 1 (bases 1 to 484)  
Tsang, S.  
Gene expression in seed germination in Brassica napus  
Unpublished (2004)  
Contact: Ed Tsang  
Plant Natural Products  
National Research Council of Canada  
Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon,  
Saskatchewan, S7N 0W9, Canada  
Tel: 306 975 4164  
Fax: 306 975 4839  
Email: Ed.Tsang@nrc-cnrc.gc.ca  
High quality sequence stop: 484.  
Location/Qualifiers  
1..484  
/organism="Brassica napus"  
/mol\_type="mRNA"  
/db\_xref="taxon:3708"  
/clone\_lib="Brassica napus 3ETMS"  
/note="Vector: pDNR-LIB CREATOR; Site\_1: SfiIA; Site\_2: SfiIB; Sequences have been trimmed to remove vector and low quality regions using LUCY sequence cleanup software (www.tigr.org)."

FEATURES  
source

ORIGIN

Query Match 79.1%; Score 327.6; DB 7; Length 484;  
Best Local Similarity 89.9%; Pred. No. 1e-69;  
Matches 374; Conservative 0; Mismatches 39; Indels 3; Gaps 2;  
QY 1 GTTTATTAGTCATGCGCTAAGTTTGGTCGCATCATCGCACTCTTTTGTCTCTTT 60  
|||||  
DB 51 GTATTACTAGTGAGCATGCGCTAAGTTTGTCTTCCCATCATTTGCCCCACTTTTGTCTCTTT 110  
|||||

QY 61 GTTCTTTTTCGCTTTCGAAGCACCACCAATCGTGGAGCAGACGAAGTTGTGCGAAGG 120  
 Db 111 GTTCTTTTTCGCTTTCGAAGCACCACCAATCGTGGAGCAGACGAAGTTGTGCGAAGG 170  
 QY 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAACAATAACGCATGCAAGAAATCAGTGCATT 180  
 Db 171 CCAAGTGGGACATGGTCAGGAGTCTGTGGAACAATAACGCATGCAAGAAATCAGTGCATT 230  
 QY 181 AACCTTGAGAAAGCAGACATGGATCTTGCACATATGCTTCCAGCTCACAAGTGTATC 240  
 Db 231 AACCTTGAGAAAGCAGACATGGATCTTGCACATATGCTTCCAGCTCACAAGTGTATC 290  
 QY 241 TGTCTACTTTCCCTTGTAAATTTATCGCAAACTCTTTGGTGAATAGTTTATGTAATTTAC 300  
 Db 291 TGTCTACTTTCCCTTGTAAATTTATCGCAAACTCTTTGGTGAATAGTTTATGTAATTTAC 350  
 QY 301 ACAAATAAGTCAGTGTCTACTATCCATGAGTGATTTTAAGACATGTACC--AGATATGTT 358  
 Db 351 ACAAATAAGTCAGTGTCTACTATCCATGAGTGATTTTAAGACATGTACC--AGATATGTT 410  
 QY 359 ATGTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAA 414  
 Db 411 ATGTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAA 465

RESULT 2  
 CN726625 547 bp mRNA linear EST 14-MAY-2005  
 LOCUS 3BTMS UP 006 C09 10JUN2003\_038 Brassica napus 3BTMS Brassica napus  
 DEFINITION cDNA 5', mRNA sequence.

ACCESSION CN726625  
 VERSION CN726625.1 GI:65284427  
 KEYWORDS EST.

SOURCE Brassica napus (rape)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 547)

Teang, E.

Gene expression in seed germination in Brassica napus

Unpublished (2004)

Contact: Ed Teang

Plant Natural Products

National Research Council of Canada

Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon,

Saskatchewan, S7N 0W9, Canada

Tel: 306 975 4164

Fax: 306 975 4839

Email: Ed.teang@nrc-cnrc.gc.ca

High quality sequence stop: 547.

Location/Qualifiers

FEATURES

source

1..547

/organism="Brassica napus"

/mol\_type="mRNA"

/db\_xref="taxon:3708"

/clone\_lib="Brassica napus 3BTMS"

/notes="Vector: pDNR-LIB CREATOR; Site\_1: SfiI; Site\_2:

SfiI; Sequences have been trimmed to remove vector and

low quality regions using LUCY sequence cleanup software

(www.tigr.org)."

ORIGIN

Query Match 78.9%; Score 326.8; DB 7; Length 547;  
 Best Local Similarity 88.2%; Pred. No. 1.6e-69;  
 Matches 367; Conservative 0; Mismatches 47; Indels 2; Gaps 1;

QY 1 GTTTTATTAGTATCATGGTAAGTTTGGCTCCATCATCGCACTTTCTTTTGGCTGCTCTT 60

Db 48 GTATTACTAGTACGATGGTAAGTTTGGCTTCCATCATGCCCCCACTTTTGTGCTCTT 107

QY 61 GTTCTTTTTCGCTTTCGAAGCACCACCAATCGTGGAGCAGACGAAGTTGTGCGAAGG 120

Db 108 GTTCTTTTTCGCTTTCGAAGCACCACCAATCGTGGAGCAGACGAAGTTGTGCGAAGG 167  
 QY 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAACAATAACGCATGCAAGAAATCAGTGCATT 180  
 Db 168 CCAAGTGGGACATGGTCAGGAGTCTGTGGAACAATAACGCATGCAAGAAATCAGTGCATT 227  
 QY 181 AACCTTGAGAAAGCAGACATGGATCTTGCACATATGCTTCCAGCTCACAAGTGTATC 240  
 Db 228 AACCTTGAGAAAGCAGACATGGATCTTGCACATATGCTTCCAGCTCACAAGTGTATC 287  
 QY 241 TGTCTACTTTCCCTTGTAAATTTATCGCAAACTCTTTGGTGAATAGTTTATGTAATTTAC 300  
 Db 288 TGTCTACTTTCCCTTGTAAATTTATCGCAAACTCTTTGGTGAATAGTTTATGTAATTTAC 347  
 QY 301 ACAAATAAGTCAGTGTCTACTATCCATGAGTGATTTTAAGACATGTACC--AGATATGTT 358  
 Db 348 ACAAATAAGTCAGTGTCTACTATCCATGAGTGATTTTAAGACATGTACC--AGATATGTT 407  
 QY 359 ATGTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAA 414  
 Db 408 ATGTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAA 463

RESULT 3

CN725823

LOCUS

DEFINITION

napus cDNA 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Brassica napus (rape)

Brassica napus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 566)

Fei, H., Li, F., Tsang, E. and Cutler, A.

Gene expression in germinating and dormant seeds of Brassica napus

Unpublished (2004)

Contact: Adrian Cutler

National Research Council of Canada

Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon,

Saskatchewan, S7N 0W9, Canada

Tel: 306 975 5581

Fax: 306 975 4839

Email: Adrian.Cutler@nrc-cnrc.gc.ca

High quality sequence stop: 566.

Location/Qualifiers

FEATURES

source

1..566

/organism="Brassica napus"

/mol\_type="mRNA"

/db\_xref="taxon:3708"

/clone\_lib="Brassica napus 17ACDHMS"

/note="Vector: pDNR-LIB CREATOR; Site\_1: Sfi IA; Site\_2:

Sfi IB; Sequences have been trimmed to remove vector and

low quality regions using LUCY sequence cleanup software

(www.tigr.org)."

ORIGIN

Query Match 78.7%; Score 326; DB 7; Length 566;  
 Best Local Similarity 89.7%; Pred. No. 2.5e-69;  
 Matches 373; Conservative 0; Mismatches 40; Indels 3; Gaps 2;

QY 1 GTTTTATTAGTATCATGGTAAGTTTGGCTCCATCATCGCACTTTCTTTTGGCTGCTCTT 60

Db 49 GTATTACTAGTACGATGGTAAGTTTGGCTTCCATCATGCCCCCACTTTTGTGCTCTT 108

QY 61 GTTCTTTTTCGCTTTCGAAGCACCACCAATCGTGGAGCAGACGAAGTTGTGCGAAGG 120

Db 109 GTTCTTTTTCGCTTTCGAAGCACCACCAATCGTGGAGCAGACGAAGTTGTGCGAAGG 168

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QY 121 CCAAGTGGGACATGGTCCAGGAGTCTGTGGAAACAATAACGCATGCAAGAAATCAGTGCATT 180
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DB 169 CCAAGTGGGACATGGTCCAGGAGTCTGTGGAAACAATAACGCATGCAAGAAATCAGTGCATT 228
    |||
QY 181 AACCTTGAGAAAGCAGACATGGATCTTCCAACTATGTCTTCCAGCTCACAAGTGTATC 240
    |||
DB 229 AACCTTGAGAAAGCAGACATGGATCTTCCAACTATGTCTTCCAGCTCACAAGTGTATC 288
    |||
QY 241 TGTACTCTTCCCTTGTAAATTTATCGCAAACTCTTTGGTGAATAGTTTATGTAATTTAC 300
    |||
DB 289 TGTACTCTTCCCTTGTAAATTTATCGCAAACTCTTTGGTGAATAGTTTATGTAATTTAC 348
    |||
QY 301 ACAAAATAGTCAGTGTCACTATCCATGAGTGAATTTAAGACATGTACC--AGATATGTT 358
    |||
DB 349 ATAAAAAATAGTCGTGTCACTATCAATGAGTGAATTTATGACATGTACCTGATATATGTT 408
    |||
QY 359 ATGTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAAATAAAAAA 414
    |||
DB 409 ATGTTGGTTCGGTTATA-ATAAAAGTTTATGACACCGTAAAAAATAAAAAA 463
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RESULT 4
CN726272
LOCUS 3ETMS UP_002_A11_10JUN2003_048 Brassica napus 3ETMS Brassica napus
DEFINITION CDNA 5', mRNA sequence.
ACCESSION CN726272
VERSION CN726272.1 GI:65284074
KEYWORDS EST.
SOURCE Brassica napus (rape)
ORGANISM Brassica napus

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 484)
AUTHORS Tsang,E.
TITLE Gene expression in seed germination in Brassica napus
JOURNAL Unpublished (2004)
COMMENT Contact: Ed Tsang
Plant Natural Products
National Research Council of Canada
Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon,
Saskatchewan, S7N 0W9, Canada
Tel: 306 975 4164
Fax: 306 975 4839
Email: Ed.Tsang@nrc-cnrc.gc.ca
High quality sequence stop: 484.
Location/Qualifiers
1..484
/organism="Brassica napus"
/mol_type="mRNA"
/db_xref="taxon:3708"
/clone_lib="Brassica napus 3ETMS"
/notes="Vector: pDNR-LIB_CREATOR; Site_1: SfIIA; Site_2:
SfiIB; Sequences have been trimmed to remove vector and
low quality regions using LUCY sequence cleanup software
(www.tigr.org)."

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FEATURES
source

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1..484
/organism="Brassica napus"
/mol_type="mRNA"
/db_xref="taxon:3708"
/clone_lib="Brassica napus 3ETMS"
/notes="Vector: pDNR-LIB_CREATOR; Site_1: SfIIA; Site_2:
SfiIB; Sequences have been trimmed to remove vector and
low quality regions using LUCY sequence cleanup software
(www.tigr.org)."

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## ORIGIN

```

Query Match 78.4%; Score 324.4; DB 7; Length 484;
Best Local Similarity 89.4%; Pred. No. 6.3e-69;
Matches 372; Conservative 0; Mismatches 41; Indels 3; Gaps 2;

QY 1 GTTTTATTAGTATGATGCTAAGTTTGGTCCATCATCGCACTCTTTTCTGCTCTT 60
    |||
DB 51 GTATTACTAGTGAGCATGGCTAAGTTTGTCTTCATCATTTGCCCACTTTTCTGCTCTT 110
    |||
QY 61 GTTCTTTTGTGCTCTTTTGAAGCACCACCAATGGTGAAGCAGAGAAGTTTGGCGAAGG 120
    |||
DB 111 GTTCTTTTGTGCTCTTTTGAAGCACCACCAATGGTGAAGCAGAGAAGTTTGGCGAAGG 170
    |||
QY 121 CCAAGTGGGACATGGTCCAGGAGTCTGTGGAAACAATAACGCATGCAAGAAATCAGTGCATT 180
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DB 171 CCAAGTGGGACATGGTCCAGGAGTCTGTGGAAACAATAACGCATGCAAGAAATCAGTGCATT 230
    |||
QY 181 AACCTTGAGAAAGCAGACATGGATCTTCCAACTATGTCTTCCAGCTCACAAGTGTATC 240
    |||
DB 231 AACCTTGAGAAAGCAGACATGGATCTTCCAACTATGTCTTCCAGCTCACAAGTGTATC 290
    |||
QY 241 TGTACTCTTCCCTTGTAAATTTATCGCAAACTCTTTGGTGAATAGTTTATGTAATTTAC 300
    |||
DB 291 TGTACTCTTCCCTTGTAAATTTATCGCAAACTCTTTGGTGAATAGTTTATGTAATTTAC 350
    |||
QY 301 ACAAAATAGTCAGTGTCACTATCCATGAGTGAATTTAAGACATGTACC--AGATATGTT 358
    |||
DB 351 ATAAAAAATAGTCGTGTCACTATCAATGAGTGAATTTTGTGACATGTACCTGATATATGTT 410
    |||
QY 359 ATGTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAAATAAAAAA 414
    |||
DB 411 ATGTTGGTTCGGTTATA-ATAAAAGTTTATGACACCGAATAAAAAAATAAAAAA 465
    |||

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## RESULT 5

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CN726374
LOCUS 3ETMS UP_003_C06_10JUN2003_022 Brassica napus 3ETMS Brassica napus
DEFINITION CDNA 5', mRNA sequence.
ACCESSION CN726374
VERSION CN726374.1 GI:65284176
KEYWORDS EST.
SOURCE Brassica napus (rape)
ORGANISM Brassica napus

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 485)
AUTHORS Tsang,E.
TITLE Gene expression in seed germination in Brassica napus
JOURNAL Unpublished (2004)
COMMENT Contact: Ed Tsang
Plant Natural Products
National Research Council of Canada
Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon,
Saskatchewan, S7N 0W9, Canada
Tel: 306 975 4164
Fax: 306 975 4839
Email: Ed.Tsang@nrc-cnrc.gc.ca
High quality sequence stop: 485.
Location/Qualifiers
1..485
/organism="Brassica napus"
/mol_type="mRNA"
/db_xref="taxon:3708"
/clone_lib="Brassica napus 3ETMS"
/notes="Vector: pDNR-LIB_CREATOR; Site_1: SfIIA; Site_2:
SfiIB; Sequences have been trimmed to remove vector and
low quality regions using LUCY sequence cleanup software
(www.tigr.org)."

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FEATURES
source

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1..485
/organism="Brassica napus"
/mol_type="mRNA"
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/clone_lib="Brassica napus 3ETMS"
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SfiIB; Sequences have been trimmed to remove vector and
low quality regions using LUCY sequence cleanup software
(www.tigr.org)."

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## ORIGIN

```

Query Match 78.4%; Score 324.4; DB 7; Length 485;
Best Local Similarity 89.4%; Pred. No. 6.3e-69;
Matches 372; Conservative 0; Mismatches 41; Indels 3; Gaps 2;

QY 1 GTTTTATTAGTATGATGCTAAGTTTGGTCCATCATCGCACTCTTTTCTGCTCTT 60
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DB 52 GTATTACTAGTGAGCATGGCTAAGTTTGTCTTCATCATTTGCCCACTTTTCTGCTCTC 111
    |||
QY 61 GTTCTTTTGTGCTCTTTTGAAGCACCACCAATGGTGAAGCAGAGAAGTTTGGCGAAGG 120
    |||
DB 112 GTTCTTTTGTGCTCTTTTGAAGCACCACCAATGGTGAAGCAGAGAAGTTTGGCGAAGG 171
    |||
QY 121 CCAAGTGGGACATGGTCCAGGAGTCTGTGGAAACAATAACGCATGCAAGAAATCAGTGCATT 180
    |||
DB 172 CCAAGTGGGACATGGTCCAGGAGTCTGTGGAAACAATAACGCATGCAAGAAATCAGTGCATT 231
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QY 181 AACCTTGAGAAAGCAGCATGATCTTGCACATATGCTTCCAGCTCACAAAGTGATC 240  
 Db 232 AACCTTGAGAAAGCAGCATGATCTTGCACATATGCTTCCAGCTCACAAAGTGAT 291  
 QY 241 TGCTACTTTCCTTGTAAATTTATCGAAACTCTTTGGTGAATAGTTTATGTAATTTAC 300  
 Db 292 TGCTACTTTCCTTGTAACTCATCGCCAACTCTTTGGTGGTGTAGTTTGTGTAATTTAC 351  
 QY 301 ACAAAATAAGTCAGTGCTACTATCCATGAGTGAATTTTAAGACATGTACC--AGATATGTT 358  
 Db 352 ATAAAAAAGTCGTGCTCACTATCAATGAGTGATTTTATGACATGTACCTGTATATGTT 411  
 QY 359 ATGTTGGTTCGGTTATACAAATAAAGTTTTATTCACCAAAAAAATAAAAAA 414  
 Db 412 ATGTTGGTTCGGTTATA-ATAAAAAGTTTTATGACCAATAAAAAAATAAAAAA 466

RESULT 6  
 LOCUS CN726255  
 DEFINITION 3ETMS UP\_001\_H06\_10JUN2003\_017 Brassica napus 3ETMS Brassica napus  
 cDNA 5', mRNA sequence.  
 ACCESSION CN726255  
 VERSION CN726255.1 GI:65284057  
 KEYWORDS EST.  
 SOURCE Brassica napus (rape)  
 ORGANISM Brassica napus  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
 REFERENCE 1 (bases 1 to 481)  
 AUTHORS Tsang,E.  
 TITLE Gene expression in seed germination in Brassica napus  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: Ed Tsang  
 Plant Natural Products  
 National Research Council of Canada  
 Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon,  
 Saskatchewan, S7N 0W9, Canada  
 Tel: 306 975 4164  
 Fax: 306 975 4839  
 Email: Ed.Tsang@nrc-cnrc.gc.ca  
 High quality sequence stop: 481.

FEATURES  
 source  
 1..481  
 /organism="Brassica napus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3708"  
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 /note="Vector: pDNR-LIB-CREATOR; Site\_1: SfIIA; Site\_2:  
 SfiIB; Sequences have been trimmed to remove vector and  
 low quality regions using LUCY sequence cleanup software  
 (www.tigr.org)."  
 ORIGIN

Query Match 78.0%; Score 322.8; DB 7; Length 481;  
 Best Local Similarity 89.2%; Pred. No. 1.5e-68;  
 Matches 371; Conservative 0; Mismatches 42; Indels 3; Gaps 2;  
 QY 1 GTTTTATTAGTGATCATGGCTAAGTTTGGCTCATCATCGACTCTCTTTTGGTGTCTT 60  
 Db 51 GTATTACTAGTGAGCAGCGTAAAGTTTGGTTCATCATATTGCCCATCTTTTGGTGTCTT 110  
 QY 61 GTTCTTTTGTCTCTTTCGAAGCACCACCAATCGTGGAGCA CAGAAGTTGTGCGAAAGG 120  
 Db 111 GTTCTTTTGTCTCTTTCGAAGCACCACCAATCGTGGAGCA CAGAAGTTGTGCGAGAGG 170  
 QY 121 CCAAGTGGGACATGGTTCAGAGTCTGTGGAAACAATAACCGATGCAAGATCAGTGCATT 180  
 Db 171 CCAAGTGGGACATGGTTCAGAGTCTGTGGAAACAATAACCGATGCAAGATCAGTGCATT 230  
 QY 181 AACCTTGAGAAAGCAGCATGATCTTGCACATATGCTTCCAGCTCACAAAGTGATC 240

Db 231 AACCTTGAGAAAGCAGCATGATCTTGCACATATGCTTCCAGCTCACAAAGTGAT 290  
 QY 241 TGCTACTTTCCTTGTAAATTTATCGAAACTCTTTGGTGAATAGTTTATGTAATTTAC 300  
 Db 291 TGCTACTTTCCTTGTAACTCATCGCCAACTCTTTGGTGGTGTAGTTTGTGTAATTTAC 350  
 QY 301 ACAAAATAAGTCAGTGCTACTATCCATGAGTGAATTTTAAGACATGTACC--AGATATGTT 358  
 Db 351 ATAAAAAAGTCGTGCTCACTATCAATGAGTGAATTTTATGACATGTACCTGTATATGTT 410  
 QY 359 ATGTTGGTTCGGTTATACAAATAAAGTTTTATTCACCAAAAAAATAAAAAA 414  
 Db 411 ATGTTGGTTCGGTTATA-ATAAAAAGTTTTATGCGCAAAAAAATAAAAAA 465

RESULT 7  
 LOCUS CN726661  
 DEFINITION 3ETMS UP\_006\_G02\_10JUN2003\_002 Brassica napus 3ETMS Brassica napus  
 cDNA 5', mRNA sequence.  
 ACCESSION CN726661  
 VERSION CN726661.1 GI:65284463  
 KEYWORDS EST.  
 SOURCE Brassica napus (rape)  
 ORGANISM Brassica napus  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
 REFERENCE 1 (bases 1 to 456)  
 AUTHORS Tsang,E.  
 TITLE Gene expression in seed germination in Brassica napus  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: Ed Tsang  
 Plant Natural Products  
 National Research Council of Canada  
 Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon,  
 Saskatchewan, S7N 0W9, Canada  
 Tel: 306 975 4164  
 Fax: 306 975 4839  
 Email: Ed.Tsang@nrc-cnrc.gc.ca  
 High quality sequence stop: 456.

FEATURES  
 source  
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 /organism="Brassica napus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3708"  
 /clone\_lib="Brassica napus 3ETMS"  
 /note="Vector: pDNR-LIB-CREATOR; Site\_1: SfIIA; Site\_2:  
 SfiIB; Sequences have been trimmed to remove vector and  
 low quality regions using LUCY sequence cleanup software  
 (www.tigr.org)."  
 ORIGIN

Query Match 77.3%; Score 320; DB 7; Length 456;  
 Best Local Similarity 87.9%; Pred. No. 7.5e-68;  
 Matches 364; Conservative 0; Mismatches 40; Indels 10; Gaps 1;  
 QY 1 GTTTTATTAGTGATCATGGCTAAGTTTGGCTCATCATCGACTCTCTTTTGGTGTCTT 60  
 Db 36 GTATTACTAGTGATCATGGCTAAGTTTGGCTTCATCATTTGCCCTACTTTTGGTGTCTT 95  
 QY 61 GTTCTTTTGTCTCTTTCGAAGCACCACCAATCGTGGAGCA CAGAAGTTGTGCGAAAGG 120  
 Db 96 GTCTTTTTCGTCTCTTCGAAGCACCACCAATCGTGGAGCA CAGAAGTTGTGCGAGAGG 155  
 QY 121 CCAAGTGGGACATGGTTCAGAGTCTGTGGAAACAATAACCGATGCAAGATCAGTGCATT 180  
 Db 156 CCAAGTGGGACATGGTTCAGAGTCTGTGGAAACAATAACCGATGCAAGATCAGTGCATT 215  
 QY 181 AACCTTGAGAAAGCAGCATGATCTTGCACATATGCTTCCAGCTCACAAAGTGATC 240  
 Db 216 AACCTTGAGAAAGCAGCATGATCTTGCACATATGCTTCCAGCTCACAAAGTGAT 275

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QY 241 TGCTACTTTCCTGTGTAATTAATCGCAAACTCTTTGGTGAATAGTTTTTTATGTAATTTAC 300
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Db 276 TGCTACTTCCCTGTGTAATTAATCGCAAACTCTTTGGTGGTGTAGTTTTGTGTAATTTAC 335
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QY 301 ACAAAATAGTCAGTGTCACTATCCATGAGTGAATTTTAAGACATGTACCAGATATGTTAT 360
    |||||
Db 336 ATAAATAAGTCTGTGTCACTATCAATGAGTGAATTTTATGACATGTACCTGATATGTTAT 395
    |||||
QY 361 GTTGGTTCGGTTATACAAATAAAGTTTTTATTCACCAAAAAAAAAAAAAAAAAAAAA 414
    |||||
Db 396 GTTATAATATAAAGTTTTTATGCACCTGAAAAAATAAAAAAAAAAAAAAAAAAAAA 449
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RESULT 8
CN726701          458 bp  mRNA  linear  EST 14-MAY-2005
LOCUS             3ETMS UP_007_B11_11JUN2003_047 Brassica napus 3ETMS Brassica napus
DEFINITION        cDNA 5', mRNA sequence.
ACCESSION         CN726701
VERSION           CN726701.1 GI:65284503
KEYWORDS          EST.
SOURCE            Brassica napus (rape)
ORGANISM          Brassica napus
                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
                  rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE         1 (bases 1 to 458)
AUTHORS           Tsang,E.
TITLE             Gene expression in seed germination in Brassica napus
JOURNAL           Unpublished (2004)
COMMENT           Contact: Ed Tsang
                  Plant Natural Products
                  National Research Council of Canada
                  Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon,
                  Saskatchewan, S7N 0W9, Canada
                  Tel: 306 975 4164
                  Fax: 306 975 4839
                  Email: Ed.Tsang@nrc-cnrc.gc.ca
                  High quality sequence stop: 458.
FEATURES          source
                  1..458
                  /organism="Brassica napus"
                  /mol_type="mRNA"
                  /db_xref="taxon:3708"
                  /clone_lib="Brassica napus 3ETMS"
                  /note="Vector: pDNR-LIB_CREATOR; Site_1: SfIIA; Site_2:
                  SfiIB; Sequences have been trimmed to remove vector and
                  low quality regions using LUCY sequence cleanup software
                  (www.tigr.org)."

ORIGIN
Query Match      76.4%; Score 316.4; DB 7; Length 458;
Best Local Similarity 85.3%; Pred. No. 5.7e-87;
Matches 353; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 1 GTTTATTAGTATCATGGCTAAGTTTGGTCCATCATCGCACTCTCTTTTGTGCTCTTT 60
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Db 36 GTATTACTAGTATCATGGCTAAGTTTGGTCCATCATTTGCCCTACTTTTGTGCTCTTT 95
    |||||
QY 61 GTTCTTTTGTCTCTTCGAAGCACCAACAATGGTGGAGACAGAGAAGTTGTGCGAAAGG 120
    |||||
Db 96 GTCCTTTTGTCTCTCTCGAAGCACCAACAATGGTGGAGACAGAGAAGTTGTGCGAGAGG 155
    |||||
QY 121 CCAAGTGGGACATGGTCAGAGTCTGTGGAAACAATAACGCATGCAAGATCAGTGCATT 180
    |||||
Db 156 CCAAGTGGGACATGGTCAGAGTCTGTGGAAACAATAACGCATGCAAGATCAGTGCATT 215
    |||||
QY 181 AACCTTGAGAAAGCAGACATGGATCTTGCAACTATGTCTTCCAGCTCACAGTGTATC 240
    |||||
Db 216 AACCTTGAGAAAGCAGACATGGATCTTGCAACTATGTCTTCCAGCTCACAGTGTAT 275
    |||||
QY 241 TGCTACTTTCCTGTGTAATTAATCGCAAACTCTTTGGTGAATAGTTTTTTATGTAATTTAC 300
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Db 276 TGCTACTTCCCTGTGTAATTAATCGCAAACTCTTTGGTGGTGTAGTTTTGTGTAATTTAC 335
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QY 301 ACAAAATAGTCAGTGTCACTATCCATGAGTGAATTTTAAGACATGTACCAGATATGTTAT 360
    |||||
Db 336 ATAAATAAGTCTGTGTCACTATCAATGAGTGAATTTTATGACATGTACCTGATATGTTAT 395
    |||||
QY 361 GTTGGTTCGGTTATACAAATAAAGTTTTTATTCACCAAAAAAAAAAAAAAAAAAAAA 414
    |||||
Db 396 GTTATAATATAAAGTTTTTATGCACCTGAAAAAATAAAAAAAAAAAAAAAAAAAAA 449
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RESULT 9
CN726329          597 bp  mRNA  linear  EST 14-MAY-2005
LOCUS             3ETMS UP_002_G01_10JUN2003_002 Brassica napus 3ETMS Brassica napus
DEFINITION        cDNA 5', mRNA sequence.
ACCESSION         CN726329
VERSION           CN726329.1 GI:65284131
KEYWORDS          EST.
SOURCE            Brassica napus (rape)
ORGANISM          Brassica napus
                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
                  rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE         1 (bases 1 to 597)
AUTHORS           Tsang,B.
TITLE             Gene expression in seed germination in Brassica napus
JOURNAL           Unpublished (2004)
COMMENT           Contact: Ed Tsang
                  Plant Natural Products
                  National Research Council of Canada
                  Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon,
                  Saskatchewan, S7N 0W9, Canada
                  Tel: 306 975 4164
                  Fax: 306 975 4839
                  Email: Ed.Tsang@nrc-cnrc.gc.ca
                  High quality sequence stop: 597.
FEATURES          source
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                  /organism="Brassica napus"
                  /mol_type="mRNA"
                  /db_xref="taxon:3708"
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                  SfiIB; Sequences have been trimmed to remove vector and
                  low quality regions using LUCY sequence cleanup software
                  (www.tigr.org)."

ORIGIN
Query Match      76.2%; Score 315.6; DB 7; Length 597;
Best Local Similarity 88.6%; Pred. No. 9.1e-67;
Matches 365; Conservative 0; Mismatches 44; Indels 3; Gaps 2;

QY 1 GTTTATTAGTATCATGGCTAAGTTTGGTCCATCATCGCACTCTCTTTTGTGCTCTTT 60
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Db 51 GTATTACTAGTATGAGCATGGCTAAGTTTGGTCTTCATCATTTGCCCCCACTTTTGTGCTCTTT 110
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QY 61 GTTCTTTTGTCTCTTCGAAGCACCAACAATGGTGGAGACAGAGAAGTTGTGCGAAAGG 120
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Db 111 GTCTTTTGTCTCTTCGAAGCACCAACAATGGTGGAGACAGAGAAGTTGTGCGAGAGG 170
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QY 121 CCAAGTGGGACATGGTCAGAGTCTGTGGAAACAATAACGCATGCAAGATCAGTGCATT 180
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Db 171 CCAAGTGGGACATGGTCAGAGTCTGTGGAAACAATAACGCATGCAAGATCAGTGCATT 230
    |||||
QY 181 AACCTTGAGAAAGCAGACATGGATCTTGCAACTATGTCTTCCAGCTCACAGTGTATC 240
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Db 231 AACCTTGAGAAAGCAGACATGGATCTTGCAACTATGTCTTCCAGCTCACAGTGTAT 290
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QY 241 TGCTACTTTCCTGTGTAATTAATCGCAAACTCTTTGGTGAATAGTTTTTTATGTAATTTAC 300
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Db 291 TGCTACTTCCCTGTGTAATTAATCGCAAACTCTTTGGTGGTGTAGTTTTGTGTAATTTAC 350
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QY 301 ACAAATAAGTCAGTGTCTACTATCCATGAGTGATTTTAAACATGTACC--AGATATGTT 358
Db 351 ATAAATAAGTCGTGTCTACTATCAATGAGTGATTTTATGACATGACCTGATATGTT 410
QY 359 ATGTCGGTTCGGTTATACAAATAAAGTTTATTACCAAAAAAATAAAAAA 410
Db 411 AATGTCGGTTCGGTTATA-ATAAATAAGTTTATGACCCGTAAATAAGATATA 461

RESULT 10
CN726424
LOCUS
DEFINITION
3ETMS UP_003_H02_10JUN2003_001 Brassica napus 3ETMS Brassica napus
CDNA 5', mRNA sequence.
CN726424
CN726424.1 GI:65284226
EST.
Brassica napus (rape)
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 453)
Tsang,E.
Gene expression in seed germination in Brassica napus
Unpublished (2004)
Contact: Ed Tsang
Plant Natural Products
National Research Council of Canada
Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon,
Saskatchewan, S7N 0W9, Canada
Tel: 306 975 4164
Fax: 306 975 4839
Email: Ed.Tsang@nrc-cnrc.gc.ca
High quality sequence stop: 453.
FEATURES
source
1..453
Location/Qualifiers
/organism="Brassica napus"
/mol_type="mRNA"
/db_xref="taxon:3708"
/clone_lib="Brassica napus 3ETMS"
/notes="Vector: pDNR-LIB CREATOR; Site 1: SfIIA; Site 2:
SfiIB; Sequences have been trimmed to remove vector and
low quality regions using LUCY sequence cleanup software
(www.tigr.org)."
ORIGIN
Query Match 76.1%; Score 315.2; DB 7; Length 453;
Best Local Similarity 87.2%; Pred. No. 1.1e-66;
Matches 361; Conservative 0; Mismatches 43; Indels 10; Gaps 1;
QY 1 GTTTTATTAGTGATCGCTAAGTTTGGCTCCATCATCGCACTCTTTTGGTCTCTT 60
Db 36 GTATTACTAGTGATCGCTAAGTTTGGCTCCATCATTCGCCCTACTTTTGGTCTCTT 95
QY 61 GTTCTTTTGGCTCTTTCGAGCACCACCAATGGTGGAGGACAGAGTTGCGGAAAG 120
Db 96 GTCTTTTTCGCTCTCGAAGCACCACCAATGGTGGAGGACAGAGTTGCGGAGAG 155
QY 121 CCAAGTGGGACATGGTCAGAGTCTGTGGAACAATAACGCATGCAAGATCAGTGCATT 180
Db 156 CCAAGTGGGACATGGTCAGAGTCTGTGGAACAATAACGCATGCAAGATCAGTGCATT 215
QY 181 AACCTTTGAGAAAGCAGACATGGATCTTGCAACTATGTCTTCCAGCTCACAAGTGATC 240
Db 216 AACCTTTGAGAAAGCAGACATGGATCTTGCAACTATGTCTTCCAGCTCACAAGTGAT 275
QY 241 TGTACTTTCTTTGTTAATTTATCGCAAACTCTTTGGTGAATAGTTTTATGTAATTTAC 300
Db 276 TGTACTTCCCTTTGTTAATTTATCGCAAACTCTATGTTGGTGGTGGTGGTGGTGGTGG 335
QY 301 ACAAATAAGTCAGTGTCTACTATCCATGAGTGATTTTAAACATGTATGATATGTTAT 360

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Db 336 ATAAATAAGTCGTGTCTACTATCAATGAGTGATTTTATGACATGACCTGATATGTTAT 395
QY 361 GTTGTTCGGTTATACAAATAAAGTTTATTACCAAAAAAATAAAAAA 414
Db 396 GTT-----ATAATATAAAGTTTATATACAAAAAATAAAAAAATAAAAAA 439

RESULT 11
CN826227
LOCUS
DEFINITION
EL1386 Brassica embryo library (EL) Brassica napus cDNA clone
EL1386 complete, mRNA sequence.
CN826227
CN826227.1 GI:65296011
EST.
Brassica napus (rape)
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 413)
Sharpe,A.G., Gjetva,J., Durkin,J. and Lydiate,D.J.
Brassica napus ESTs
Unpublished (2004)
Contact: Sharpe, A.G.
Molecular Genetics
Agriculture & Agri-Food Canada
107 Science Place, Saskatoon, Saskatchewan, Canada, S7N0X2
Tel: 306 956 7271
Fax: 306 956 7247
Email: sharpea@agr.gc.ca
Seq primer: M13 Forward and T7.
Location/Qualifiers
1..413
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/cultivar="DH12075 (double haploid line from Cresor x
Westar cross)"
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/clone_lib="EL1386"
/dev_stage="Mid to late embryos (4-6 mg)"
/lab_host="E. coli Electromax DH5 alpha-e"
/clone_lib="Brassica embryo library (EL)"
/notes="Organ: Embryos without seed coat; Vector: pSPOR11
(modified: GCGCCGCC*GACTAGTGCCTC*cgagcgcgggtcgac);
Site 1: NotI; Site 2: SalI; Seeds were collected by Dr.
Francois Ouellet when they were still very green (mid to
large stage, cotyledons were formed). The seed coats were
removed and the remaining tissue was used for cDNA library
construction. mRNA was poly-A primed using SuperScript
Plasmid System cDNA Synthesis and Cloning kit (Invitrogen)
After initial screening, the most abundant redundant
clones were screened out using 22 oligos designed to match
napins (including albumins), cruciferins, oleosins,
trypsin inhibitor 2, cytosolic GAPDH, cyclophilins, HSP70,
desaturase, and CAB (LHCP)."
ORIGIN
Query Match 75.8%; Score 313.8; DB 7; Length 413;
Best Local Similarity 87.3%; Pred. No. 2.5e-66;
Matches 359; Conservative 0; Mismatches 42; Indels 10; Gaps 1;
QY 1 GTTTTATTAGTGATCGCTAAGTTTGGCTCCATCATCGCACTCTTTTGGTCTCTT 60
Db 13 GTATTACTAGTGATCGCTAAGTTTGGCTCCATCATTCGCCCTACTTTTGGTCTCTT 72
QY 61 GTTCTTTTGGCTCTTTCGAGCACCACCAATGGTGGAGGACAGAGTTGTCGAAAG 120
Db 73 GTCTTTTTCGCTCTCGAAGCACCACCAATGGTGGAGGACAGAGTTGTCGAGAG 132
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QY      301  ACAAATAAGTCAGTGTCACTATCCATGAGTGTGATTTTAAAGACATGTACC--AGATATGTT 358
Db      373  ATAAAATAAGTCGTGTCACTATCAATGAGTGAATTTATGACATGTACCTGATATATGTT 432
QY      359  ATGTTGGTTCGGTTATACAAATAAAGTTTTATTACCA 396
Db      433  ATGTTGGTTCGGTTATA-ATAAAAGTTTTATGCACCA 469

RESULT 14
LOCUS   CD834068
DEFINITION   BN45.040H17F011019 BN45 Brassica napus cDNA clone BN45040H17, mRNA
SEQUENCE
CD834068
VERSION   CD834068.1 GI:32516008
KEYWORDS   EST.
SOURCE     Brassica napus (rape)
ORGANISM   Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1 (bases 1 to 446)
AUTHORS   Genoplante.
TITLE     Genoplante, a major partnership french program in plant genomics
JOURNAL   Unpublished (2003)
COMMENT   Contact: Genoplante
          93, rue Henri Rochefort 91025 EVRY CEDEX France
          Tel: 33 1 69 47 54 00
          Fax: 33 1 69 47 54 10
          This sequence has been generated in the framework of the french
          plant genomics programme 'Genoplante' (http://www.genoplante.com
          and http://genoplante-info.infobiogen.fr).
FEATURES   source
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Best Local Similarity 89.2%; Pred. No. 1.2e-65;
Matches 347; Conservative 0; Mismatches 40; Indels 2; Gaps 1;

QY      1  GTTTTATTAGTCATGCGCTAAGTTTGGTCCATCATCGCACTCTCTTTTGTGCTCTT 60
Db      51  GTATTACTAGTGAGCATGGCTAAGTTTGGTTCATCATTTGCCCACTTTTGTGCTCTT 110
QY      61  GTTCTTTTGTCTCTTTCGAAGCACCAAAATGGTGGAGCACAGAAAGTTTGGCGAAGG 120
Db      111  GTTCTTTTGTCTCTTTCGAAGCACCAAAATGGTGGAGCACAGAAAGTTTGGCGAAGG 170
QY      121  CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 180
Db      171  CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 230
QY      181  AACCTTGAGAAACGACAGATGATCTTGCACATATGTCTTCCAGCTCACAGTGTATC 240
Db      231  AACCTTGAGAAACGACAGATGATCTTGCACATATGTCTTCCAGCTCACAGTGTAT 290
QY      241  TGTCTCTTCTTGTGTTAAATTTATCGCAAACTCTTTGGTGAATGTTTTATGTAATTTAC 300
Db      291  TGTCTCTTCTTGTGTTAACTTATGCGCAAACTCTTTGGTGGTAGTTTGTGTAAATTTAC 350
QY      301  ACAAATAAGTCAGTGTCACTATCCATGAGTGAATTTTAAAGACATGTACC--AGATATGTT 358
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Db      351  ATAAAATAAGTCGTGTCACTATCAATGAGTGAATTTTATGACATGTACCTGATATATGTT 410
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Db      411  ATGTTGGTTCGGTTATATAAAAAAGTTT 439

RESULT 15
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DEFINITION   BN40.061003F011227 BN40 Brassica napus cDNA clone BN40061003, mRNA
SEQUENCE
CD832071
VERSION   CD832071.1 GI:32514011
KEYWORDS   EST.
SOURCE     Brassica napus (rape)
ORGANISM   Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1 (bases 1 to 452)
AUTHORS   Genoplante.
TITLE     Genoplante, a major partnership french program in plant genomics
JOURNAL   Unpublished (2003)
COMMENT   Contact: Genoplante
          93, rue Henri Rochefort 91025 EVRY CEDEX France
          Tel: 33 1 69 47 54 00
          Fax: 33 1 69 47 54 10
          This sequence has been generated in the framework of the french
          plant genomics programme 'Genoplante' (http://www.genoplante.com
          and http://genoplante-info.infobiogen.fr).
FEATURES   source
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            /clone_lib="BN40"
ORIGIN
Query Match      75.1%; Score 311; DB 6; Length 452;
Best Local Similarity 89.2%; Pred. No. 1.2e-65;
Matches 347; Conservative 0; Mismatches 40; Indels 2; Gaps 1;

QY      1  GTTTTATTAGTCATGCGCTAAGTTTGGTCCATCATCGCACTCTCTTTTGTGCTCTT 60
Db      55  GTATTACTAGTGAGCATGGCTAAGTTTGGTTCATCATTTGCCCACTTTTGTGCTCTT 114
QY      61  GTTCTTTTGTCTCTTTCGAAGCACCAAAATGGTGGAGCACAGAAAGTTTGGCGAAGG 120
Db      115  GTTCTTTTGTCTCTTTCGAAGCACCAAAATGGTGGAGCACAGAAAGTTTGGCGAAGG 174
QY      121  CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 180
Db      175  CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATT 234
QY      181  AACCTTGAGAAACGACAGATGATCTTGCACATATGTCTTCCAGCTCACAGTGTATC 240
Db      235  AACCTTGAGAAACGACAGATGATCTTGCACATATGTCTTCCAGCTCACAGTGTAT 294
QY      241  TGTCTCTTCTTGTGTTAAATTTATCGCAAACTCTTTGGTGAATGTTTTATGTAATTTAC 300
Db      295  TGTCTCTTCTTGTGTTAACTTATGCGCAAACTCTTTGGTGGTAGTTTGTGTAAATTTAC 354
QY      301  ACAAATAAGTCAGTGTCACTATCCATGAGTGAATTTTAAAGACATGTACC--AGATATGTT 358
Db      355  ATAAAATAAGTCGTGTCACTATCAATGAGTGAATTTTATGACATGTACCTGATATATGTT 414
QY      359  ATGTTGGTTCGGTTATACAAATAAAGTTT 387
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Db 415 ATGTTGGTTCGGTTATAATAAAGTTTT 443

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Job time : 3758 secs

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GenCore version 5.1.1.8  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search using frame\_plus.p2n model

Run on: May 10, 2006, 05:46:44 ; Search time 3626 Seconds  
(without alignments)  
1881.195 Million cell updates/sec

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Perfect score: 441  
Sequence: 1 MAKFASIIALLFAALVLFPA.....RHGSCNYVPPAHKCIYPPC 80

Scoring table: BLOSUM62  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0  
  
Searched: 5883141 seqs, 28421725653 residues  
  
Total number of hits satisfying chosen parameters: 11766282  
  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl.\*  
1: gb.ba.\*  
2: gb.in.\*  
3: gb.env.\*  
4: gb.om.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pr.\*  
9: gb.ro.\*  
10: gb.sts.\*  
11: gb.sv.\*  
12: gb.un.\*  
13: gb.vi.\*  
14: gb.hcg.\*  
15: gb.pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length	Description
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2	441	100.0	285 6 AR432393 Sequence
3	441	100.0	288 6 A39553 Sequence

4	441	100.0	288 6 AR050161 Sequence
5	441	100.0	288 6 AR130280 Sequence
6	441	100.0	288 6 I23736 Sequence 58
7	433	98.2	285 6 AR014692 Sequence
8	433	98.2	285 6 AR432392 Sequence
9	433	98.2	395 15 RSU18557
10	433	98.2	414 6 A26875
11	433	98.2	414 6 A39549
12	433	98.2	414 6 A63404
13	433	98.2	414 6 AR050153 Sequence
14	433	98.2	414 6 AR130272 Sequence
15	433	98.2	414 6 I23728 Sequence 48
16	433	98.2	414 6 AR207337 Sequence
17	433	98.2	414 6 AR374914 Sequence
18	433	98.2	414 6 AR642703 Sequence
19	431	97.7	449 6 E34290
20	426	96.6	575 6 BD223249 Method of
21	425	96.4	457 15 RSU18556
22	405	91.8	243 15 AY998243
23	398	90.2	243 6 BD174927
24	398	90.2	414 6 E31545
25	398	90.2	414 15 AB012871
26	396.5	89.9	451 15 BNU59459
27	396	89.8	499 15 R5AF4
28	395.5	89.7	475 15 R5BFP3
29	394	89.3	243 6 AX412329
30	394	89.3	243 6 AX412502
31	394	89.3	243 6 AX507351
32	394	89.3	243 6 AX590057
33	394	89.3	274 15 AY133787
34	394	89.3	400 6 A68647
35	394	89.3	454 15 AY063779
36	393	89.1	243 6 BD174928
37	393	89.1	363 15 AF528180
38	393	89.1	416 6 E31546
39	393	89.1	416 15 AB012872
40	388	88.0	243 6 AX412406
41	388	88.0	243 6 AX412601
42	388	88.0	243 6 AX651878
43	388	88.0	243 15 AY060506
44	388	88.0	403 6 A68645
45	388	88.0	403 15 ATANTSPEC

ALIGNMENTS

RESULT 1	AR014693	Sequence 17 from patent US 5773696.	285 bp	DNA	linear	PAT 05-DEC-1998
LOCUS	AR014693					
DEFINITION	AR014693					
ACCESSION	AR014693.1	GI:3972147				
VERSION	AR014693.1					
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 285)					
AUTHORS	Liang,J., Shah,D.Maganlal., Wu,Y.Shun. and Rosenberger,C.Annette.					
TITLE	Antifungal polypeptide and methods for controlling plant pathogenic fungi					
JOURNAL	Patent: US 5773696-A 17 30-JUN-1998;					
FEATURES	Location/Qualifiers					
source	1..285					
	/organism="unknown"					
	/mol_type="unassigned DNA"					
ORIGIN						
Alignment Scores:						
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Best Local Similarity:	100.0%	Mismatches:	0			
Query Match:	100.0%	Indels:	0			

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DB: 6 Gaps: 0
US-09-759-584-59 (1-80) x AR014693 (1-285)

Qy 1 MetAlaLysPheAlaSerIleIleAlaLeuPheAlaAlaLeuValLeuPheAlaAla 20
Db 31 ATGGCTAAGTTTGGTCCATCATCGCACCCTCTTTGCTGCTCTGCTCTCTTTGCTGCT 90
Qy 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTTP 40
Db 91 TTCGAGGCACCAACTATGTGTGGAGGCACAAAAGTTGTGCCAAGGCCATCAGGGACTTGG 150
Qy 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
Db 151 TCAGGAGTCTGCGGAACCAACACGCGATGCAAGACCAATGATCGACTCGAGAGGCA 210
Qy 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
Db 211 CGGCATGGATCTTGCAACTAGCTTTCCAGCTCACAAGTGATCTGCTACTTTCCATGC 270

RESULT 2
AR432393 LOCUS
DEFINITION Sequence 17 from patent US 6653280.
ACCESSION AR432393
VERSION AR432393.1 GI:40194670
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 285)
AUTHORS Liang,J., Shah,D.M., Wu,Y.S. and Rosenberger,C.A.
TITLE Antifungal polypeptide AlyAPP from Alyssum and methods for
controlling plant pathogenic fungi
JOURNAL Patent: US 6653280-A 17 25-NOV-2003;
Monsanto Technology LLC; St. Louis, MO
FEATURES
source
1..285
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
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Score: 441.00 Matches: 80
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-09-759-584-59 (1-80) x AR432393 (1-285)

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Qy 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTTP 40
Db 91 TTCGAGGCACCAACTATGTGTGGAGGCACAAAAGTTGTGCCAAGGCCATCAGGGACTTGG 150
Qy 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
Db 151 TCAGGAGTCTGCGGAACCAACACGCGATGCAAGACCAATGATCGACTCGAGAGGCA 210
Qy 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
Db 211 CGGCATGGATCTTGCAACTAGCTTTCCAGCTCACAAGTGATCTGCTACTTTCCATGC 270

RESULT 3
AR432393 LOCUS
DEFINITION Sequence 41 from Patent WO9416076.
ACCESSION AR432393
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VERSION A39553.1 GI:2295844
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 288)
AUTHORS Dubock,A.C., Powell,K.A. and Rees,S.B.
TITLE ANTIMICROBIAL-PROTEIN-PRODUCING ENDOSYMBIOTIC MICROORGANISMS
JOURNAL Patent: WO 9416076-A 41 21-JUL-1994;
ZENECA LTD (GB)
COMMENT Other publication AU 5820494 940815.
FEATURES
Location/Qualifiers
source
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN
Alignment Scores: 4,47e-44 Length: 288
Score: 441.00 Matches: 80
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-09-759-584-59 (1-80) x A39553 (1-288)

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Qy 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTTP 40
Db 103 TTCGAAGCACCAACCAATGTGTGAAGCAGACAGAGTTGTGCCAAGGCCAAGTGGACATGG 162
Qy 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
Db 163 TCAGGAGTCTGTGGAACCAATTAACGATGCAAGATCAGTGCATTAGACTTCGAGAAAGCA 222
Qy 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
Db 223 CGCATGTGATCTTGCAACTATGCTTCCAGCTCACAAGTGATCTGCTACTTTCTCTTGT 282

RESULT 4
AR050161 LOCUS
DEFINITION Sequence 58 from patent US 5824869.
ACCESSION AR050161
VERSION AR050161.1 GI:5972153
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 288)
AUTHORS Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,
Terras,P.R.G. and Vanderleyden,J.
TITLE Bioicidal proteins
JOURNAL Patent: US 5824869-A 58 20-OCT-1998;
LOCATION/Qualifiers
source
1..288
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores: 4,47e-44 Length: 288
Score: 441.00 Matches: 80
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0
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RESULT 6			
123736	123736	288 bp	DNA
LOCUS	Sequence 58 from patent US 5538525.		linear
DEFINITION			
ACCESSION	123736		
VERSION	123736.1	GI:1603606	
KEYWORDS	.		
SOURCE	Unknown.		

Qy		1 MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla
Db	31	ATGGCTAAGTTTGGCTCCATCATCGCACTCCTCTTTTGCTGCTCTGGTTCCTCTTTGCTGCT



QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
Db 195 CGACATGATCTTGCACACTATGCTTCCAGCTCACAAGTATCTGCTACTTCTCTGT 254

## RESULT 10

A26875 LOCUS 414 bp DNA linear PAT 30-NOV-2001  
DEFINITION R.sativus APF1 gene.  
ACCESSION A26875  
VERSION A26875.1 GI:1247352  
KEYWORDS  
SOURCE Raphanus sativus (radish)  
ORGANISM Raphanus sativus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Raphanus.

## REFERENCE 1 (bases 1 to 414)

AUTHORS Broekaert,W.F., Cammue,B.P.A., Terras,F.R.G., Vanderleyden,J.,  
Osborn,R.W. and Rees,S.B.

## TITLE BIOCIDAL PROTEINS

JOURNAL Patent: WO 9305153-A 33 18-MAR-1993;  
ICI PLC (GB)

## FEATURES

Location/Qualifiers

1..414

/organism="Raphanus sativus"

/mol\_type="unassigned DNA"

/db\_xref="taxon:3726"

## ORIGIN

Alignment Scores: Pred. No.: 6.27e-43 Length: 414  
Score: 433.00 Matches: 78  
Percent Similarity: 98.8% Conservative: 1  
Best Local Similarity: 97.5% Mismatches: 1  
Query Match: 98.2% Indels: 0  
DB: 6 Gaps: 0

US-09-759-584-59 (1-80) x A26875 (1-414)

QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20  
Db 16 ATGGCTAAGTTTGGCTCCATCATCGCACTCTTTTGTGCTCTTGTCTTTTGTCTGT 75

QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40  
Db 76 TTCGAAGCACCACCAATGGTGGAGGCACAGAGTGTGGAAAGGCCAAGTGGGACATGG 135

QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60  
Db 136 TCAGGAGTCTGTGGAAACAATACGCATGCAAGATCAGTGCAATTAACCTTGAGAAAGCA 195

QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
Db 196 CGACATGATCTTGCACACTATGCTTCCAGCTCACAAGTATCTGCTACTTCTCTGT 255

## RESULT 11

A39549 LOCUS 414 bp DNA linear PAT 05-MAR-1997  
DEFINITION Sequence 37 from Patent WO9416076.  
ACCESSION A39549  
VERSION A39549.1 GI:2295842  
KEYWORDS  
SOURCE unidentified  
ORGANISM unclassified sequences.

## REFERENCE 1 (bases 1 to 414)

AUTHORS Dubock,A.C., Powell,K.A. and Rees,S.B.

## TITLE ANTIMICROBIAL-PROTEIN-PRODUCING ENDOSYMBIOTIC MICROORGANISMS

JOURNAL Patent: WO 9416076-A 37 21-JUL-1994;

ZENECA LTD (GB)

COMMENT Other publication AU 5820494 940815.

## FEATURES

Location/Qualifiers

1..414

source

/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"

## ORIGIN

Alignment Scores: Pred. No.: 6.27e-43 Length: 414  
Score: 433.00 Matches: 78  
Percent Similarity: 98.8% Conservative: 1  
Best Local Similarity: 97.5% Mismatches: 1  
Query Match: 98.2% Indels: 0  
DB: 6 Gaps: 0

US-09-759-584-59 (1-80) x A39549 (1-414)

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Db 16 ATGGCTAAGTTTGGCTCCATCATCGCACTCTTTTGTGCTCTTGTCTTTTGTCTGT 75

QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40  
Db 76 TTCGAAGCACCACCAATGGTGGAGGCACAGAGTGTGGAAAGGCCAAGTGGGACATGG 135

QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60  
Db 136 TCAGGAGTCTGTGGAAACAATACGCATGCAAGATCAGTGCAATTAACCTTGAGAAAGCA 195

QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
Db 196 CGACATGATCTTGCACACTATGCTTCCAGCTCACAAGTATCTGCTACTTCTCTGT 255

## RESULT 12

A63404 LOCUS 414 bp DNA linear PAT 12-MAR-1998  
DEFINITION Sequence 19 from Patent WO9721814.  
ACCESSION A63404  
VERSION A63404.1 GI:3717176  
KEYWORDS  
SOURCE unidentified  
ORGANISM unclassified sequences.

## REFERENCE 1

AUTHORS Broekaert,W.F., De,S.G., Rees and Sarah,B.

TITLE ANTI-FUNGAL PROTEINS

JOURNAL Patent: WO 9721814-A 19 19-JUN-1997;

ZENECA LTD (GB)

COMMENT Other publication AU 1105397 19970703.

## FEATURES

Location/Qualifiers

1..414

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/db\_xref="taxon:32644"

## ORIGIN

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Best Local Similarity: 97.5% Mismatches: 1  
Query Match: 98.2% Indels: 0  
DB: 6 Gaps: 0

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QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20

Db 16 ATGGCTAAGTTTGGCTCCATCATCGCACTCTTTTGTGCTCTTGTCTTTTGTCTGT 75

QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40  
Db 76 TTCGAAGCACCACCAATGGTGGAGGCACAGAGTGTGGAAAGGCCAAGTGGGACATGG 135

QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60

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Db 136 TCAGGAGTCTGTGGAAACATAACCGCATCGAAGATCAGTGCATTAAACCTTGGAAAGCA 195
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Db 196 CGACATGGATCTTGCACACTATGTCTTCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255

RESULT 13
AR050153
LOCUS AR050153 414 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 48 from patent US 5824869.
ACCESSION AR050153
VERSION AR050153.1 GI:5972145
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 414)
AUTHORS Broekaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B.,
TITLE Biocidal proteins
JOURNAL Patent: US 5824869-A 48 20-OCT-1998;
FEATURES Location/Qualifiers
source 1..414
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 6.27e-43 Length: 414
Score: 433.00 Matches: 78
Percent Similarity: 98.8% Conservatives: 1
Best Local Similarity: 97.5% Mismatches: 1
Query Match: 98.2% Indels: 0
DB: Gaps: 0

US-09-759-584-59 (1-80) x AR050153 (1-414)
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Db 16 ATGGCTAAGTTTGGTCCATCATCGCACTTCTTTTGGCTGCTCTTCTTTTGGCTGT 75
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTyr 40
Db 76 TTCGAAGCACCACCAATCGTGGAGCACAGAAGTTGTGCGAAGGCCAAGTGGGACATGG 135
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
Db 136 TCAGGAGTCTGTGGAAACATAACCGCATCGAAGATCAGTGCATTAAACCTTGGAAAGCA 195
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
Db 196 CGACATGGATCTTGCACACTATGTCTTCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255

RESULT 14
AR130272
LOCUS AR130272 414 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 48 from patent US 6187904.
ACCESSION AR130272
VERSION AR130272.1 GI:14118169
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 414)
AUTHORS Broekaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B.,
TITLE Biocidal proteins
JOURNAL Patent: US 6187904-A 48 13-FEB-2001;
FEATURES Location/Qualifiers
source 1..414
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
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Score: 433.00 Matches: 78
Percent Similarity: 98.8% Conservatives: 1
Best Local Similarity: 97.5% Mismatches: 1
Query Match: 98.2% Indels: 0
DB: Gaps: 0

US-09-759-584-59 (1-80) x AR050153 (1-414)
QY 1 MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20
Db 16 ATGGCTAAGTTTGGTCCATCATCGCACTTCTTTTGGCTGCTCTTCTTTTGGCTGT 75
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTyr 40
Db 76 TTCGAAGCACCACCAATCGTGGAGCACAGAAGTTGTGCGAAGGCCAAGTGGGACATGG 135
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
Db 136 TCAGGAGTCTGTGGAAACATAACCGCATCGAAGATCAGTGCATTAAACCTTGGAAAGCA 195
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
Db 196 CGACATGGATCTTGCACACTATGTCTTCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255

RESULT 15
AR130272
LOCUS AR130272 414 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 48 from patent US 5538525.
ACCESSION AR130272
VERSION AR130272.1 GI:1603598
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 414)
AUTHORS Broekaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B.,
TITLE Biocidal proteins
JOURNAL Patent: US 5538525-A 48 23-JUL-1996;
FEATURES Location/Qualifiers
source 1..414
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 6.27e-43 Length: 414
Score: 433.00 Matches: 78
Percent Similarity: 98.8% Conservatives: 1
Best Local Similarity: 97.5% Mismatches: 1
Query Match: 98.2% Indels: 0
DB: Gaps: 0

US-09-759-584-59 (1-80) x I23728 (1-414)
QY 1 MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20
Db 16 ATGGCTAAGTTTGGTCCATCATCGCACTTCTTTTGGCTGCTCTTCTTTTGGCTGT 75
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTyr 40
Db 76 TTCGAAGCACCACCAATCGTGGAGCACAGAAGTTGTGCGAAGGCCAAGTGGGACATGG 135
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
Db 136 TCAGGAGTCTGTGGAAACATAACCGCATCGAAGATCAGTGCATTAAACCTTGGAAAGCA 195
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
Db 196 CGACATGGATCTTGCACACTATGTCTTCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
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Db 196 CGACATGGATCTTGCACACTATGTCTTCCAGCTCACAGTGTATCTGCTACTTCTTCTTGT 255

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Maximum Match 100%  
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SUMMARIES

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6	433	98.2	414	2	AAT68696	Aat68696 Radish an
7	431	97.7	449	3	AA53190	Aa53190 Raphanus
8	426	96.6	575	3	AAZ99339	Aaz99339 DNA encod
9	423	95.9	394	10	ADC51221	Adc51221 Brassica
10	423	95.9	394	13	ADU71300	Adu71300 Brassica
11	416	94.3	426	10	ADC51223	Adc51223 Brassica
12	416	94.3	426	13	ADU71302	Adu71302 Brassica
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28	387.5	87.9	286	2	AAT94574	Aat94574 Alyssum s
29	387.5	87.9	481	2	AAT99289	Aat99289 Alyssum s
30	386	87.5	308	2	AAT94577	Aat94577 Cloned 5'
31	375	85.0	500	2	AAT94581	Aat94581 Composite
32	350	79.4	1973	3	AAC46924	Aac46924 Arabidops
33	349	79.1	1616	2	AAV10646	Aav10646 A. thalia
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36	312	70.7	987	10	ADG32350	Adg32350 DNA encod
37	312	70.7	987	10	ADG32348	Adg32348 DNA encod
38	311	70.5	534	3	AAZ99327	Aaz99327 DNA encod
39	309.5	70.2	522	3	AAZ99324	Aaz99324 DNA encod
40	309	70.1	485	3	AAZ99333	Aaz99333 DNA encod
41	309	70.1	1093	3	AAZ99334	Aaz99334 DNA encod
42	308	69.8	534	3	AAZ51396	Aaz51396 Portion o
43	308	69.8	534	3	AAZ99325	Aaz99325 DNA encod
44	308	69.8	606	3	AAZ99326	Aaz99326 DNA encod
45	301	68.3	153	13	ADR39338	Adr39338 Defensin-

ALIGNMENTS

RESULT 1  
AAQ38652  
ID AAQ38652 standard; DNA; 261 BP.  
XX  
AC AAQ38652;  
DT 25-MAR-2003 (revised)  
DT 07-JUL-1993 (first entry)  
XX  
DE Rs-APP2 cDNA.  
KW Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria;  
KW fungicide; bactericide; antibiotic; antifungal; gram positive;  
KW plant disease resistance; low toxicity.  
XX  
OS Raphanus sativus.  
XX  
FH Key Location/Qualifiers  
FT CDS 16..256  
FT /\*tag= a  
XX  
PN WO9305153-A1.  
PD 18-MAR-1993.  
XX  
XX 27-AUG-1992; 92MO-GB001570.  
XX  
XX 29-AUG-1991; 91GB-00018523.  
PR

```

PR 13-FEB-1992; 92GB-00003038.
PR 25-JUN-1992; 92GB-00013526.
XX
XX (ICIL ) IMPERIAL CHEM IND PLC.
XX
XX Broekaert WF, Cammue BPA, Osborn RW, Rees SB, Terras FRG;
PI Vanderleyden J;
XX
XX WPI; 1993-100978/12.
XX
XX Biocidal proteins isolated from seeds of plants - e.g. brassica or
PT dahlia, useful for increasing plants' resistance to fungal and bacterial
PT diseases.
PT
XX
XX Example 21; Fig 35; 110pp; English.
XX
XX This cDNA represents the sequence of Rs-APP2 from Raphanus sativus. PCR
CC primer AAQ38640 was used together with AAQ38641 to generate a probe for
CC screening a Raphanus sativus seed cDNA library. This primer corresponds
CC to amino acids 2 to 7 of Rs-APP1 and has a sense orientation. The 144bp
CC product was partially re-amplified using AAQ38642 and AAQ38641 to give a
CC 123bp product, which was further reamplified with the same primers and
CC digoxigenin-11-dUTP instead of dTTP to give a digoxigenin labeled PCR
CC product. This was used to screen a lambda ZAPII cDNA library by in situ
CC plaque hybridisation. Positive plaques were purified and subjected to two
CC additional screening rounds with the same probe. Inserts were excised in
CC vivo into the pBluescript phagemid form with the aid of helper phage
CC R408. Inserts from 22 positive clones were excised by EcoRI digestion and
CC their size compared by agarose gel electrophoresis. Four clones had
CC insert sizes of approx. 400bp the others between 250-300bp. The inserts
CC of the 4 largest clones were then sequenced and found to differ only in
CC the length of their 5' and 3' UTR's. The longest sequence was identified
CC as Rs-APP1 (AAQ38650). Rs-APP2 was seen to differ by only 2 amino acids
CC from Rs-APP1, so the Rs-APP1 cDNA was transformed to the Rs-APP2
CC nucleotide sequence by PCR assisted site directed mutagenesis. (Updated
CC on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 261 BP; 67 A; 55 C; 59 G; 80 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8-76e-45 Length: 261
Score: 441.00 Matches: 80
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-09-759-584-59 (1-80) x AAQ38652 (1-261)
QY 1 MetAlaIyPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20
DB 16 ATGGCTTAAGTTTGGGTCCATCATCGCACTTCTTTTGTGCTCTTCTTTTGTGCTGT 75
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
DB 76 TTCGAGCACCACCAATGTTGGTGAAGCACAGAAAGTTGTGCCAAAGGCCAAGTGGGACATGG 135
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
DB 136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAAATCAGTGCATTAGACTTGAAGAAGCA 195
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
DB 196 CGACATGGATCTTGGCAACTATGTTCTCCAGCTCACAAAGTATCTGCTACTTCTTCTTGT 255

RESULT 2
AAQ70130
ID AAQ70130 standard; cDNA; 288 BP.
XX
XX AAQ70130;
XX
XX 25-MAR-1993 (revised)
DT 14-FEB-1995 (first entry)
DT

XX Antimicrobial Rs-APP2.
DE
XX
XX Antimicrobial; Rs-APP2; symbiosis; disease-resistance; fungus-resistance;
KW Clavibacter xyli subsp. cynodontis; Cxc; crop improvement; endophyte;
KW PCR; polymerase chain reaction; mutagenesis; ss.
XX
XX Raphanus sativus.
OS
XX
XX WO9416076-A1.
PN
XX
XX 21-JUL-1994.
XX
XX 05-JAN-1994; 94WO-GB0000012.
XX
XX 08-JAN-1993; 93GB-00000281.
PR
XX (ZENE ) ZENECA LTD.
PA
XX
XX Dubock AC, Powell KA, Rees SB;
PI
XX
XX WPI; 1994-249223/30.
DR
XX P-PSDB; AAR57327.
DR
XX
XX Antimicrobial protein producing endo-symbiotic microorganisms - is
PT produced by combining nucleic acids encoding the protein with an
PT endophyte, useful for protecting plant hosts from esp. fungal disease.
PT
XX Disclosure; Page 33; 39pp; English.
XX
XX Plant-derived antimicrobial proteins are expressed in endosymbiotic
CC Clavibacter xyli subsp. cynodontis (Cxc). Plants or seeds treated with
CC recombinant Cxc are protected against fungal disease. A suitable
CC antimicrobial protein is Rs-APP1 from R. sativus. The full-length cDNA
CC sequence of PCR assisted site-directed mutagenesis of Rs-APP2 is given in
CC AAQ70130 and the deduced amino acid sequence in AAR57327. (Updated on 25-
CC MAR-2003 to correct PN field.)
XX
XX Sequence 288 BP; 70 A; 66 C; 69 G; 83 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1e-44 Length: 288
Score: 441.00 Matches: 80
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-09-759-584-59 (1-80) x AAQ70130 (1-288)
QY 1 MetAlaIyPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20
DB 43 ATGGCTTAAGTTTGGGTCCATCATCGCACTTCTTTTGTGCTCTTCTTTTGTGCTGT 102
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
DB 103 TTCGAGCACCACCAATGTTGGTGAAGCACAGAAAGTTGTGCCAAAGGCCAAGTGGGACATGG 162
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
DB 163 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAAATCAGTGCATTAGACTTGAAGAAGCA 222
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
DB 223 CGACATGGATCTTGGCAACTATGTTCTCCAGCTCACAAAGTATCTGCTACTTCTTCTTGT 282

RESULT 3
AAQ38650
ID AAQ38650 standard; DNA; 414 BP.
XX
XX AAQ38650;
XX
XX 25-MAR-2003 (revised)
DT

```

— 178 —

QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60  
 Db 136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGATCAGTGCATTAAACCTTGAGAAAGCA 195

QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
 Db 196 CGACATGGATCTTGGCAACTATGCTTCCAGCTCACAGTGTATCTGCTACTTCTTCTTGT 255

RESULT 5  
 AAT72333  
 ID AAT72333 standard; cDNA; 414 BP.  
 XX  
 AC AAT72333;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 19-JAN-1998 (first entry)  
 XX  
 DE Raphanus sativus antifungal protein I (Rs-APPI) cDNA.  
 XX  
 KW Antifungal protein; candida; fungal resistance; food additive; radish;  
 KW crop protection; plant defensin; bacterial protection; preservative; ss.  
 XX  
 OS Raphanus sativus.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 16..258  
 FT /\*tag= a  
 FT /transl\_except= (pos:85..87, aa:Glu)  
 FT sig\_peptide 16..102  
 FT /\*tag= b  
 FT mat\_peptide 103..255  
 FT /\*tag= c  
 FT /product= "antifungal\_protein\_1"  
 FT  
 FT  
 XX WO9721815-A2.  
 XX  
 XX 19-JUN-1997.  
 PD  
 XX  
 XX 12-DEC-1996; 96WO-GB003068.  
 XX  
 XX 13-DEC-1995; 95GB-00025455.  
 PR 28-MAR-1996; 96GB-00006552.  
 XX  
 XX (ZENE ) ZENECA LTD.  
 PA  
 XX Meloen RH, Puijk WC, Schaaper WM, Sijtsma L, Van Amerongen A;  
 PI Broekaert W, Samblanx GW, Fant F, Borremans FAM, Rees SB;  
 PI Van Gelder WMJ;  
 XX  
 XX WPI; 1997-332786/30.  
 DR P-PSDB; AAW19280.  
 DR  
 XX  
 XX Antifungal peptide derived from radish antifungal protein 2 - and related  
 PT DNA, useful for producing plants with increased fungal resistance and as  
 PT therapeutic or preservative agent.  
 PT  
 XX  
 XX Claim 8; Fig 2; 65pp; English.  
 XX  
 XX This cDNA sequence encodes an Raphanus sativus (radish) antifungal  
 CC protein (Rs-APPI). Analogues of the homologous protein, Rs-APP2  
 CC (AAW19281), have also been produced (see AAW19282-92, AAW19294-98,  
 CC AAW19301-04, AAW1930-34 and AAW31765-834). Plants containing DNA  
 CC sequences encoding these proteins have improved resistance to fungi.  
 CC Compositions containing the peptides can be used to control fungi or  
 CC bacteria in pharmaceutical (e.g. treatment of Candida infections) or  
 CC preservative purposes (as food additives). In agriculture, the peptide  
 CC may be used to improve disease resistance or disease tolerance of crops,  
 CC either pre or post harvest. When applied to plants they may also have  
 CC curative as well as protective actions. The peptides may also be used to  
 CC protect plants by introducing them, or a microorganism capable of  
 CC expressing the peptide into the soil. (Updated on 25-MAR-2003 to correct  
 CC PI field.)

XX  
 SQ Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1.55e-43 Length: 414  
 Score: 433.00 Matches: 78  
 Percent Similarity: 98.8% Conservative: 1  
 Best Local Similarity: 97.5% Mismatches: 1  
 Query Match: 98.2% Indels: 0  
 DB: 2 Gaps: 0

US-09-759-584-59 (1-80) x AAT72333 (1-414)  
 QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20  
 Db 16 ATGGCTAAGTTTGGCTCCATCATCGCACTTCTTTTGGCTGCTCTTTTGTCTTGT 75  
 QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40  
 Db 76 TTCGAAGCACCAACAATGGTGAAGCACAGAAAGTTGTGCGAAAGGCCCAAGTGGGACATGG 135  
 QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60  
 Db 136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGATCAGTGCATTAAACCTTGAGAAAGCA 195  
 QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
 Db 196 CGACATGGATCTTGGCAACTATGCTTCCAGCTCACAGTGTATCTGCTACTTCTTCTTGT 255

RESULT 6  
 AAT68696  
 ID AAT68696 standard; cDNA; 414 BP.  
 XX  
 AC AAT68696;  
 XX  
 DT 13-DEC-1997 (first entry)  
 XX  
 DE Radish antifungal protein 1 (Rs-APPI) cDNA.  
 XX  
 KW Rs-APPI; radish antifungal protein 1; fungicide; salt tolerance;  
 KW preservative; transgenic plant; crop protection.  
 XX  
 OS Raphanus sativus.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 16..258  
 FT /\*tag= a  
 FT /transl\_except= (pos:85..87, aa:Glu)  
 FT sig\_peptide 16..102  
 FT /\*tag= b  
 FT mat\_peptide 103..255  
 FT /\*tag= c  
 FT  
 FT  
 XX WO9721814-A1.  
 PN  
 XX 19-JUN-1997.  
 PD  
 XX  
 XX 12-DEC-1996; 96WO-GB003065.  
 XX  
 XX 13-DEC-1995; 95GB-00025474.  
 PR (ZENE ) ZENECA LTD.  
 PA  
 XX Broekaert WF, De Samblanx GW, Rees SB;  
 XX WPI; 1997-332785/30.  
 DR P-PSDB; AAW19617.  
 DR  
 XX New active mutants of radish antifungal protein 2 - used to generate  
 PT fungus-resistant plants or as therapeutic or preservative agents.  
 PT  
 XX Disclosure; Fig 2; 39pp; English.  
 XX

CC This cDNA clone codes for the preprotein for the radish antifungal protein 1 (Rs-APP1) (AAW19617). Novel antifungal proteins are based on Rs-APP1, Rs-APP2 (see AAW19616), Rs-APP3 and Rs-APP4, especially those in which Gly9 is replaced by Arg, Val39 by Arg, Gly9 by Arg, Glu5 by Met and/or Gly16 by Met. Mutants (see AAW26371-90) of Rs-APP2 are specifically claimed. The CC mutants show improved salt tolerant antifungal activity, particularly CC when expressed in plants

SQ Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;

Alignment Scores: 1.55e-43 Length: 414  
 Pred. No.: 433.00 Matches: 78  
 Score: 98.8% Conservative: 1  
 Percent Similarity: 97.5% Mismatches: 0  
 Best Local Similarity: 98.2% Indels: 0  
 Query Match: 2 Gaps: 0  
 DB:

US-09-759-584-59 (1-80) x AAT68696 (1-414)

QY 1 MetAlaLysPheAlaSerIleIleAlaLeuPheAlaAlaLeuValLeuPheAlaAla 20  
 DB 16 ATGGCTAAGTTGGTCCATCATCGCACTCTTTTGGCTGCTCTTTTGGCTGCT 75  
 QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40  
 DB 76 TTCGAAGCACCACCAATGTTGGGAAGCACAGAGTTGTGCGAAGGCCAAGTGGGACATGG 135  
 QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60  
 DB 136 TCAGGAGTCTGTGGAAACCAATACGCATCGCAAGATCAAGTCAACCTTGAGAAAGCA 195  
 QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
 DB 196 CGACATGGATCTTGCACATAGTCTCCAGCTCACAAGTATCTGCTACTTCTTCTTGT 255

#### RESULT 7

AAZ53190  
 ID AAZ53190 standard; DNA; 449 BP.  
 XX  
 AC AAZ53190;  
 XX  
 DT 06-OCT-2000 (first entry)  
 XX  
 DE Raphanus sativus antibacterial protein radishin encoding DNA SEQ ID NO:1.  
 XX  
 KW Raphanus sativus; antibacterial; plant; resistance; paddy; radishin;  
 KW pathogenic microbe; radish; rice blast disease; ds.  
 XX  
 OS Raphanus sativus.  
 XX  
 JP2000116379-A.  
 XX  
 PD 25-APR-2000.  
 XX  
 PF 09-OCT-1998; 98JP-00288472.  
 XX  
 PR 09-OCT-1998; 98JP-00288472.  
 XX  
 PA (TOYA-) TOYAMA KEN.  
 XX  
 WIPI; 2000-389821/34.  
 DR P-PSDB; AAY91117.  
 XX

Isolated DNA from Raphanus sativus used to transform a microbe and a plant to produce an antibacterial protein used to increase resistance of rice paddy against pathogenic microbes.

Claim 1; Page 4; 7pp; Japanese.

The present sequence encodes an antibacterial protein, designated radishin, isolated from Raphanus sativus (radish). A phage or plasmid comprising radishin can be used for increasing resistance of paddy and

CC rice blast disease against pathogenic microbes  
 XX Sequence 449 BP; 126 A; 78 C; 94 G; 151 T; 0 U; 0 Other;

Alignment Scores: 3.04e-43 Length: 449  
 Pred. No.: 431.00 Matches: 77  
 Score: 98.8% Conservative: 2  
 Percent Similarity: 96.2% Mismatches: 1  
 Best Local Similarity: 97.7% Indels: 0  
 Query Match: 3 Gaps: 0  
 DB:

US-09-759-584-59 (1-80) x AAZ53190 (1-449)

QY 1 MetAlaLysPheAlaSerIleIleAlaLeuPheAlaAlaLeuValLeuPheAlaAla 20  
 DB 41 ATGGCTAAGTTGGTCCATCATCGCACTCTTTTGGCTGCTCTTTTGGCTGCT 100  
 QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40  
 DB 101 TTCGAAGCACCACCAATGTTGGGAAGCACAGAGTTGTGTCAGAGGCCAAGTGGGACATGG 160  
 QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60  
 DB 161 TCAGGAGTCTGTGGAAATTAATAACGATGCAAGATCAAGTCACTTGCATTCGAGAAAGCA 220  
 QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
 DB 221 CGACATGGTCTTGCACATAGTCTCCAGCTCACAAGTATCTGTTATTTCCCTTGT 280

#### RESULT 8

AAZ99339  
 ID AAZ99339 standard; DNA; 575 BP.  
 XX  
 AC AAZ99339;  
 XX  
 DT 03-JUL-2000 (first entry)  
 XX  
 DE DNA encoding a fusion protein of DmAMP1 and RsAPP2.  
 XX  
 KW Antimicrobial protein; AMP1; transgenic plant; linker peptide;  
 KW protein expression; plant defensin; RsAPP2; antifungal protein; APP2; ss.  
 XX  
 OS Synthetic.  
 OS Dahlia merckii.  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 CDS 3..566  
 FT /\*tag= a  
 FT /product= "fusion protein of DmAMP1 and RsAPP2"  
 XX  
 WO200011175-A1.  
 XX  
 PD 02-MAR-2000.  
 XX  
 PF 17-AUG-1999; 99WO-GB002716.  
 XX  
 PR 18-AUG-1998; 98GB-00018001.  
 PR 04-DEC-1998; 98GB-00026753.  
 XX  
 PA (ZENB ) ZENECA LTD.  
 XX  
 PI Broekaert WF, Francoise IEJA, De Bolle MFC, Evans IJ, Ray JA;  
 XX WIPI; 2000-246564/21.  
 DR P-PSDB; AAY84072.  
 XX  
 PT Improving expression of polyproteins in plants involves coexpression of  
 PT two or more proteins in plants within a single transcription unit.  
 XX Disclosure; Fig 34; 151pp; English.  
 XX

CC The present sequence encodes a protein of the invention, comprising the  
 CC mature proteins of the plant defensin, the Dahlia antimicrobial protein  
 CC (AMP) 1 and the antifungal protein 2 (RafP2), linked by a linker  
 CC propeptide of the invention. The specification describes methods for  
 CC improving expression levels of one or more proteins in a transgenic  
 CC plant. The method comprises inserting a DNA sequence having a promoter  
 CC region operably linked to two or more protein encoding regions separated  
 CC by a DNA sequence coding for a linker propeptide and a terminator region.  
 CC The method is used to produce proteins in plants. The linker propeptide  
 CC comprising a cleavage site, whereby the expressed polypeptide is post-  
 CC translationally processed into the component protein molecules. The  
 CC propeptide sequence is rich in amino acids A, V, S and T and contains  
 CC dipeptidic sequences consisting of either two acidic, two basic or one  
 CC acidic and one basic residue as a cleavable linker sequence  
 XX  
 SQ Sequence 575 BP; 133 A; 137 C; 149 G; 156 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 1,73e-42 Length: 575  
 Score: 426.00 Matches: 78  
 Percent Similarity: 97.5% Conservative: 0  
 Best Local Similarity: 97.5% Mismatches: 2  
 Query Match: 96.6% Indels: 0  
 DB: 3 Gaps: 0

US-09-759-584-59 (1-80) x AA299339 (1-575)

QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20  
 Db 324 ATGGCTAAGTTTGGCGTCCATCATCGCACTTCTTTTGGCTGCTTTTGGCTGCT 383  
 QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuLysLeuGlnArgProSerGlyThrTTP 40  
 Db 384 TTCAAGAGCACCACCAATGTTGGAAGCACAGAAAGTTGTGCCAAGGCCAAGTCGTACATGG 443  
 QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60  
 Db 444 TCAGGAGTCTGTGGAAACAAATACGATCGCAAGATCATGTCATAGATCTTGGAAGCA 503  
 QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
 Db 504 CGACATGGATCTTGCAACTATCGTTTCCAGCTCACAGTGTATCTGCTACTTTCCTTGT 563

RESULT 9

ADCS1221  
 ID ADCS1221 standard; DNA; 394 BP.  
 AC ADCS1221;  
 XX  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE Brassica oleracea defensin protein coding sequence.  
 XX  
 KW antimicrobial protein; defensin; transgenic plant;  
 KW composite disease resistance; pathogenic bacteria;  
 KW rice white leaf blight; brown-stripe disease; glume blight;  
 KW seedling damping-off disease; filamentous fungi; rice blight;  
 KW sheath blight disease; leaf blight; gene; ds.  
 XX  
 OS Brassica oleracea.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..243  
 FT /\*tag= a  
 FT /product= "Brassica oleracea defensin protein"

JP2003088379-A.

25-MAR-2003.

18-SEP-2001; 2001JP-00283117.

18-SEP-2001; 2001JP-00283117.

XX (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.  
 PA  
 XX WPI; 2003-621123/59.  
 DR P-PSDB; ADCS1222.  
 XX

PT Novel protein from Brassica campestris, useful as antimicrobial against  
 PT plant pathogenic filamentous fungi or pathogenic bacteria, especially for  
 PT treating e.g. rice white leaf blight and sheath blight disease.  
 XX

PS Claim 3; SEQ ID NO 1; 34pp; Japanese.

XX The invention comprises the amino acid and coding sequences of  
 CC antimicrobial (defensin) proteins from Brassica. The DNA and protein  
 CC sequences of the invention are useful for producing transformed plants  
 CC with composite disease resistance, especially resistant to diseases  
 CC caused by pathogenic bacteria, such as: rice white leaf blight, brown-  
 CC stripe disease, glume blight, and seedling damping-off disease. As well  
 CC as diseases caused by filamentous fungi, such as: rice blight, sheath  
 CC blight disease, and leaf blight. The present DNA sequence encodes a  
 CC Brassica defensin protein of the invention.

XX SQ Sequence 394 BP; 116 A; 71 C; 82 G; 125 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 2,43e-42 Length: 394  
 Score: 423.00 Matches: 76  
 Percent Similarity: 96.2% Conservative: 1  
 Best Local Similarity: 95.0% Mismatches: 3  
 Query Match: 95.9% Indels: 0  
 DB: 10 Gaps: 0

US-09-759-584-59 (1-80) x ADCS1221 (1-394)

QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20  
 Db 1 ATGGCTAAGTTTGTGCTCCATCATTCCTTCTTTTGGCTGCTTCTTTTCGCTGCT 60  
 QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuLysLeuGlnArgProSerGlyThrTTP 40  
 Db 61 CTCGAAGCACCACCAATGTTGGAAGCACAGAAAGTTGTGCGAGAGCCCAAGTGGGACATGG 120  
 QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60  
 Db 121 TCAGGAGTCTGTGGAAACAAATACGATCGCAAGATCATGTCATTAACCTTGGAAGCA 180  
 QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
 Db 181 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAGTGTATTTGCTACTTCCCTTGT 240

RESULT 10

ADU71300  
 ID ADU71300 standard; cDNA; 394 BP.

AC ADU71300;

DT 10-FEB-2005 (first entry)

DE Brassica oleracea defensin protein coding sequence - SEQ ID 1.

KW antimicrobial; plant disease resistance; gene; ss; defensin.

OS Brassica oleracea.

XX Key Location/Qualifiers  
 FT CDS 1..243  
 FT /\*tag= a  
 FT /product= "Brassica oleracea defensin protein - SEQ ID 2"

JP2004329215-A.

25-NOV-2004.

```

PF 07-JUN-2004; 2004JP-00168986.
XX
XX
PR 18-SEP-2001; 2001JP-00283117.
XX
XX
PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
XX
XX
DR WPI; 2004-809169/80.
DR P-PSDB; ADU71301.
XX
XX
PT Novel Brassica sp. derived protein having antimicrobial activity, useful
PT for producing multiple disease resistant plants.
XX
XX
PS Example 2; SEQ ID NO 1; 16pp; Japanese.
XX
XX
CC The invention comprises the amino acid and coding sequence of an
CC antimicrobial protein obtained from Brassica sp. The DNA and protein
CC sequences of the invention are useful in the production of a multiple
CC disease resistant plant. The present cDNA sequence encodes the Brassica
CC oleracea defensin protein.
XX
SQ Sequence 394 BP; 116 A; 71 C; 82 G; 125 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,43e-42 Length: 394
Score: 423.00 Matches: 76
Percent Similarity: 96.2% Conservative: 1
Best Local Similarity: 95.0% Mismatches: 3
Query Match: 95.9% Indels: 0
DB: 13 Gaps: 0

US-09-759-584-59 (1-80) x ADU71300 (1-394)
QY 1 MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20
Db 1 ATGGCTAAGTTGTGTCCATCATTTGCCCTACTTTTGTCTCTTGTCTCTTGTCTCTTGTCT 60
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
Db 61 CTCGAAGCACCACCAATGTTGGAGGCACAGAAAGTTGTGGAGAGGCCAAGTGGGACATGG 120
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
Db 121 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGATCAAGTGCATTAACCTTGAGAAAGCA 180
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
Db 181 CGACATGGATCTTGCAACTATGTCTTCCAGCTCAAGTGTATTGTCTACTTCCCTTGT 240

RESULT 11
ID ADC51223
XX ADC51223 standard; DNA; 426 BP.
XX
XX ADC51223;
XX
DT 18-DEC-2003 (first entry)
XX
XX Brassica defensin protein coding sequence.
XX
XX antimicrobial protein; defensin; transgenic plant;
XX composite disease resistance; pathogenic bacteria;
XX rice white leaf blight; brown-stripe disease; glume blight;
XX seedling damping-off disease; filamentous fungi; rice blight;
XX sheath blight disease; leaf blight; gene; ds.
XX
XX Brassica sp.
XX
XX Key Location/Qualifiers
XX CDS 1..243
XX /*tag= a
XX /product= "Brassica defensin protein"
XX
XX JP2003088379-A.

```

---

```

PD 25-MAR-2003.
XX
XX
PF 18-SEP-2001; 2001JP-00283117.
XX
XX
PR 18-SEP-2001; 2001JP-00283117.
XX
XX
PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
XX
XX
DR WPI; 2003-621123/59.
DR P-PSDB; ADC51224.
XX
XX
PT Novel protein from Brassica campestris, useful as antimicrobial against
PT plant pathogenic filamentous fungi or pathogenic bacteria, especially for
PT treating e.g. rice white leaf blight and sheath blight disease.
XX
XX
PS Claim 3; SEQ ID NO 3; 34pp; Japanese.
XX
XX
CC The invention comprises the amino acid and coding sequences of
CC antimicrobial (defensin) proteins from Brassica. The DNA and protein
CC sequences of the invention are useful for producing transformed plants
CC with composite disease resistance, especially resistant to diseases
CC caused by pathogenic bacteria, such as: rice white leaf blight, brown-
CC stripe disease, glume blight, and seedling damping-off disease. As well
CC as diseases caused by filamentous fungi, such as: rice blight, sheath
CC blight disease, and leaf blight. The present DNA sequence encodes a
CC Brassica defensin protein of the invention.
XX
SQ Sequence 426 BP; 142 A; 72 C; 84 G; 128 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.94e-41 Length: 426
Score: 416.00 Matches: 75
Percent Similarity: 95.0% Conservative: 1
Best Local Similarity: 93.8% Mismatches: 4
Query Match: 94.3% Indels: 0
DB: 10 Gaps: 0

US-09-759-584-59 (1-80) x ADC51223 (1-426)
QY 1 MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20
Db 1 ATGGCAAGTTGTGTCTATCATTTGCCCTACTTTTGTCTCTTGTCTCTTGTCTCTTGTCT 60
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
Db 61 TTCGAGGACCAACAATGTTGGAGACACAGAAAGTTGTGGAGAGGCCAAGTGGGACATGG 120
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
Db 121 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGATCAAGTGCATTAACCTTGAGAAAGCA 180
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
Db 181 CGACATGGATCTTGCAACTATGTCTTCCAGCTCAAGTGTATTGTCTACTTCCCTTGT 240

RESULT 12
ADU71302
ID ADU71302 standard; DNA; 426 BP.
XX
XX ADU71302;
XX
DT 10-FEB-2005 (first entry)
XX
XX Brassica antimicrobial protein coding sequence - SEQ ID 3.
XX
XX antimicrobial; plant disease resistance; gene; ds.
XX
XX Brassica sp.
XX
XX Key Location/Qualifiers
XX CDS 1..243
XX /*tag= a
XX /product= "Brassica antimicrobial protein - SEQ ID 4"
XX
XX

```



```
PN JP11313678-A.
XX
XX 16-NOV-1999.
XX
XX 30-APR-1998; 98JP-00121303.
XX
XX 30-APR-1998; 98JP-00121303.
XX
XX (IWAT-) IWATE KEN.
XX
XX WPI; 2000-057353/05.
XX
XX P-PSDB; AAY57564.
XX
XX
XX An antibacterial protein gene of Wasabia japonica - useful as a food- or
PT feed-additive.
XX
XX Claim 3; Page 12-13; 16pp; Japanese.
XX
XX The present sequence encodes an antibacterial protein isolated from
CC Wasabia japonica. The antibacterial protein can be used as a food or feed
CC additive. (Updated on 15-SEP-2003 to standardise OS field)
XX
XX Sequence 414 BP; 108 A; 79 C; 80 G; 147 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 2.98e-39 Length: 414
Score: 398.00 Matches: 70
Percent Similarity: 95.0% Conservative: 6
Best Local Similarity: 87.5% Mismatches: 4
Query Match: 90.2% Indels: 0
DB: 3 Gaps: 0
US-09-759-584-59 (1-80) x AA239123 (1-414)
QY 1 MetAlaLysPheAlaSerIleAlaLeuPheAlaLeuValLeuPheAlaLa 20
Db 1 ATGGCTAAGTTTGGCTTCTATCATCGCTCTTCTTCGCTGCTTCTTTCTGCT 60
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
Db 61 TTTGAAGCACCACCAATCGTGGAGCGCAGAGAGTTGTGCGAGAGTCAAGTGGGACATGG 120
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
Db 121 TCAGGAGTGTGGAAACCAACAAATCGTGCAGAGAAATCAGTGCATCAACCTTGAGGGAGCA 180
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
Db 181 CGACATGGATCTTGCACATATATCTTCCATATATCAGAGATGATCTGTACTTCCCATGT 240
RESULT 15
ID AB214241
XX AB214241 standard; DNA; 243 BP.
XX
XX AB214241;
XX
XX 21-JAN-2003 (first entry)
XX
XX Arabidopsis thaliana stress regulated gene SEQ ID NO 2046.
XX
XX Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX
XX Arabidopsis thaliana.
XX
XX WO200216655-A2.
XX
XX 28-FEB-2002.
XX
XX 24-AUG-2001; 2001WO-02026685.
XX
XX 24-AUG-2000; 2000US-0227866P.
XX
XX 26-JAN-2001; 2001US-0264647P.
XX
XX 22-JUN-2001; 2001US-0300111P.
XX
XX (SCRI ) SCRIPTS RES INST.
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
XX Harper JF, Kreps J, Wang X, Zhu T;
XX
XX WPI; 2002-304127/34.
XX
XX Identifying a stress condition to which a plant cell has been exposed and
PT producing plants with increased tolerance to these abiotic stresses.
XX
XX Claim 144; SEQ ID NO 2046; 577pp + Sequence Listing; English.
XX
XX The invention relates to identifying a stress condition to which a plant
CC cell has been exposed, comprising: (a) contacting nucleic acid
CC representative of expressed polynucleotides in the plant cell with an
CC array or probes representative of the plant cell genome; and (b)
CC detecting a profile of expressed polynucleotides in the plant cell
CC characteristic of a stress response. The method is useful in the
CC production of transgenic plants, cells and seeds and in producing plants
CC with increased tolerance to abiotic stress. The present sequence is that
CC of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used
CC in methods of the invention. Note: The sequence data for this patent is
CC not represented in the printed specification but is based on sequence
CC information supplied to Derwent by the European Patent Office
XX
XX Sequence 243 BP; 62 A; 57 C; 58 G; 66 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 4.5e-39 Length: 243
Score: 394.00 Matches: 69
Percent Similarity: 93.8% Conservative: 6
Best Local Similarity: 86.2% Mismatches: 5
Query Match: 89.3% Indels: 0
DB: 6 Gaps: 0
US-09-759-584-59 (1-80) x AB214241 (1-243)
QY 1 MetAlaLysPheAlaSerIleAlaLeuPheAlaLeuValLeuPheAlaLa 20
Db 1 ATGGCTAAGTTTGGCTTCTATCATCACCTTATCTTCGCTGCTTCTTTCTGCT 60
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
Db 61 TTCGACGCGCCGCAATCGTGGAGCAGACAGAAAGTTGTGCGAGAGCCAAAGTGGGACATGG 120
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
Db 121 TCAGGGGTTTGGCGAAACAGTAATGATGCAAGAAATCAGTGCATTAACCTTGAAGAGGCC 180
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
Db 181 AAACATGATCATGCAACTATGCTTCCAGCAGACACAGATGATCTGTATGCTCCCATGT 240
Search completed: May 10, 2006, 06:01:44
Job time : 455 secs
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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 10, 2006, 06:02:00 ; Search time 3003.5 Seconds  
(without alignments)  
1869.302 Million cell updates/sec

Title: US-09-759-584-59  
Perfect score: 441  
Sequence: 1 MAKFAIIALLFAALVLFPA.....RHGSCNYVPPAHKCIYFPC 80

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DRV=xlh  
-Q=/abes/ABSSWEB spool/US09759584/runat\_08052006\_175231\_11286/app query.fasta\_1  
-DB=EST\_QPMT-fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPECL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blomum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abes03h  
-USER=US09759584 @CGN 1.1 6731 @runat\_08052006\_175231\_11286 -NCPU=6 -ICPU=3  
-NO WMAP -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_hic:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_est7:\*  
9: gb\_gss1:\*  
10: gb\_gss2:\*  
11: gb\_gss3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length	Description
1	432	98.0	CD834852
2	432	98.0	CD833613
3	432	98.0	CD833047
4	432	98.0	CD833661
5	432	98.0	CD828840
6	428	97.1	CD833938
7	428	97.1	CD829429

8	427	96.8	413	7	CN826227	CN826227	EL1386	BR
9	427	96.8	418	6	CD832625	CD832625	BN40.064A	
10	427	96.8	420	6	CD833944	CD833944	BN45.040B	
11	427	96.8	421	6	CD826491	CD826491	BN25.064A	
12	427	96.8	421	6	CD831111	CD831111	BN40.058A	
13	427	96.8	421	6	CD833977	CD833977	BN45.040D	
14	427	96.8	422	6	CD833983	CD833983	BN45.040D	
15	427	96.8	426	6	CD827413	CD827413	BN25.067G	
16	427	96.8	438	6	CD831294	CD831294	BN40.058N	
17	427	96.8	438	6	CD831479	CD831479	BN40.059J	
18	427	96.8	453	6	CD834008	CD834008	BN45.040E	
19	427	96.8	453	7	CN726424	CN726424	3ETMS UP	
20	427	96.8	456	7	CN726661	CN726661	3ETMS UP	
21	427	96.8	480	6	CD828332	CD828332	BN25.070H	
22	427	96.8	553	6	CD831014	CD831014	BN40.047K	
23	426	96.6	376	7	CN827135	CN827135	EL2049F B	
24	426	96.6	408	6	CD833779	CD833779	BN45.001I	
25	426	96.6	409	6	CD832294	CD832294	BN40.062L	
26	426	96.6	409	6	CD834090	CD834090	BN45.040I	
27	426	96.6	446	6	CD834068	CD834068	BN45.040H	
28	426	96.6	447	6	CD832592	CD832592	BN40.063O	
29	426	96.6	450	6	CD834611	CD834611	BN45.042H	
30	426	96.6	452	6	CD832071	CD832071	BN40.061O	
31	426	96.6	458	6	CD834994	CD834994	BN45.043O	
32	426	96.6	458	7	CN827136	CN827136	EL2049R B	
33	426	96.6	470	6	CD831680	CD831680	BN40.060H	
34	426	96.6	473	6	CD834995	CD834995	BN45.043O	
35	426	96.6	481	6	CD833924	CD833924	BN45.040A	
36	426	96.6	482	6	CD833627	CD833627	BN45.001A	
37	426	96.6	484	7	CN726241	CN726241	3ETMS UP	
38	426	96.6	485	7	CN726374	CN726374	3ETMS UP	
39	426	96.6	547	7	CN726625	CN726625	3ETMS UP	
40	426	96.6	566	7	CN725823	CN725823	17ACDHMS	
41	426	96.6	592	7	CN726094	CN726094	17ACDHMS	
42	426	96.6	597	7	CN726329	CN726329	3ETMS UP	
43	424	96.1	419	6	CD834168	CD834168	BN45.040N	
44	423	95.9	543	6	CD830628	CD830628	BN40.046D	
45	422	95.7	458	7	CN726701	CN726701	3ETMS UP	

ALIGNMENTS

RESULT 1  
CD834852  
LOCUS BN45.043G08F011229 BN45 Brassica napus cDNA clone BN45043G08, mRNA  
DEFINITION linear EST 10-JUL-2003  
ACCESSION CD834852  
VERSION CD834852.1 GI:32516792  
KEYWORDS sequence.  
SOURCE EST.  
ORGANISM Brassica napus (rape)  
Brassica napus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
REFERENCE 1 (bases 1 to 425)  
AUTHORS Genoplante.  
TITLE Genoplante, a major partnership french program in plant genomics  
JOURNAL Unpublished (2003)  
COMMENT Contact: Genoplante  
Genoplante  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplante' (<http://www.genoplante.com>  
and <http://genoplante-info.infoblogen.fr>).  
FEATURES  
source  
1..425  
/organism="Brassica napus"  
/mol\_type="mRNA"  
/cultivar="Jet Neuf"  
/db\_xref="taxon:3708"

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/clone="BN45043G08"  
/tissue_type="seed"  
/clone_lib="BN45"
```

## ORIGIN

## Alignment Scores:

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Pred. No.: 1.14e-40 Length: 425  
Score: 432.00 Matches: 76  
Percent Similarity: 100.0% Conservative: 4  
Best Local Similarity: 95.0% Mismatches: 0  
Query Match: 98.0% Indels: 0  
DB: 6 Gaps: 0
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US-09-759-584-59 (1-80) x CD834852 (1-425)

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QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAa 20  
DB 49 ATGGCTAAGTTTGGCTTCCATCGTTGCCCTTCTTTCTCTGCCCTTGTATTATTTTGTGCT 108  
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTTP 40  
DB 109 TTCGAAGCACCACAAATGTTGGGAAGCACAGAAGCTGTGCAAGGCCAAGTGAACGTGG 168  
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60  
DB 169 TCAGGAGTCTGTGGAAACAATAATGATGCAAGCAATCAGTGCATTGCCTAGAGAAAGCA 228  
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
DB 229 CGACATGGATCTTGCACACTATGTCTCCAGCTCACAAGTGCATCTGCTACTTCCCTTGT 288
```

## RESULT 2

```
CD833613 427 bp mRNA linear EST 10-JUL-2003  
LOCUS BN40.067P16F011228 BN40 Brassica napus cDNA clone BN40067P16, mRNA  
DEFINITION sequence.
```

ACCESSION CD833613

VERSION CD833613.1 GI:32515553

KEYWORDS EST.

SOURCE Brassica napus (rape)

ORGANISM

Brassica napus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 427)

Genoplatte.

AUTHORS Genoplatte, a major partnership french program in plant genomics

TITLE Genoplatte, a major partnership french program in plant genomics

JOURNAL Unpublished (2003)

COMMENT Contact: Genoplatte

Genoplatte

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>  
and <http://genoplatte-info.infobiogen.fr>).

## FEATURES

source

```
1. .427  
Location/Qualifiers  
/organism="Brassica napus"  
/mol_type="mRNA"  
/cultivar="Jet Neuf"  
/db_xref="taxon:3708"  
/clone="BN40067P16"  
/tissue_type="seed"  
/clone_lib="BN40"
```

## ORIGIN

## Alignment Scores:

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Pred. No.: 1.15e-40 Length: 427  
Score: 432.00 Matches: 76  
Percent Similarity: 100.0% Conservative: 4  
Best Local Similarity: 95.0% Mismatches: 0  
Query Match: 98.0% Indels: 0
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DB: 6 Gaps: 0  
US-09-759-584-59 (1-80) x CD833613 (1-427)
```

```
QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAa 20  
DB 51 ATGGCTAAGTTTGGCTTCCATCGTTGCCCTTCTTTCTCTGCCCTTGTATTATTTTGTGCT 110  
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTTP 40  
DB 111 TTCGAAGCACCACAAATGTTGGGAAGCACAGAAGCTGTGCAAGGCCAAGTGAACGTGG 170  
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60  
DB 171 TCAGGAGTCTGTGGAAACAATAATGATGCAAGCAATCAGTGCATTGCCTAGAGAAAGCA 230  
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
DB 231 CGACATGGATCTTGCACACTATGTCTCCAGCTCACAAGTGCATCTGCTACTTCCCTTGT 290
```

## RESULT 3

CD833047

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Genoplatte.

Genoplatte, a major partnership french program in plant genomics

Unpublished (2003)

Contact: Genoplatte

Genoplatte

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>  
and <http://genoplatte-info.infobiogen.fr>).

## FEATURES

source

```
1. .449  
Location/Qualifiers  
/organism="Brassica napus"  
/mol_type="mRNA"  
/cultivar="Jet Neuf"  
/db_xref="taxon:3708"  
/clone="BN40065M05"  
/tissue_type="seed"  
/clone_lib="BN40"
```

## ORIGIN

Alignment Scores:

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Pred. No.: 1.22e-40 Length: 449  
Score: 432.00 Matches: 76  
Percent Similarity: 100.0% Conservative: 4  
Best Local Similarity: 95.0% Mismatches: 0  
Query Match: 98.0% Indels: 0  
DB: 6 Gaps: 0
```

US-09-759-584-59 (1-80) x CD833047 (1-449)

```
QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAa 20  
DB 32 ATGGCTAAGTTTGGCTTCCATCGTTGCCCTTCTTTCTCTGCCCTTGTATTATTTTGTGCT 91  
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTTP 40  
DB 92 TTCGAAGCACCACAAATGTTGGGAAGCACAGAAGCTGTGCAAGGCCAAGTGAACGTGG 151
```

QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAArgLeuGluLysAla 60  
 |||||  
 Db 152 TCAGGAGTCTGTGGAACAATAATGTCATGCAAGATCAGTGCATTCGACTAGAGAAGCA 211  
 |||||  
 QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
 |||||  
 Db 212 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAAGTGCATCTGCTACTTCCCTTGT 271  
 |||||

RESULT 4  
 CD833661  
 LOCUS  
 DEFINITION  
 BN45.001C04F010914 BN45 Brassica napus cDNA clone BN45001C04, mRNA  
 sequence.  
 ACCESSION  
 CD833661  
 VERSION  
 CD833661.1 GI:32515601  
 EST.  
 SOURCE  
 Brassica napus (rape)  
 ORGANISM  
 Brassica napus  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE  
 1 (bases 1 to 523)  
 Genoplatne.  
 AUTHORS  
 Genoplatne, a major partnership french program in plant genomics  
 TITLE  
 Unpublished (2003)  
 JOURNAL  
 COMMENT  
 Contact: Genoplatne  
 Genoplatne  
 93, rue Henri Rochefort 91025 EVRY CEDEX France  
 Tel: 33 1 69 47 54 00  
 Fax: 33 1 69 47 54 10  
 This sequence has been generated in the framework of the french  
 plant genomics programme 'Genoplatne' (<http://www.genoplatne.com>  
 and <http://genoplatne-info.infobiogen.fr>).

FEATURES  
 source  
 1..523  
 Location/Qualifiers  
 /organism="Brassica napus"  
 /mol\_type="mRNA"  
 /cultivar="Jet Neuf"  
 /db\_xref="taxon:3708"  
 /clone="BN45001C04"  
 /tissue\_type="seed"  
 /clone\_lib="BN45"

ORIGIN  
 Alignment Scores:  
 Pred. No.: 1.5e-40 Length: 523  
 Score: 432.00 Matches: 76  
 Percent Similarity: 100.0% Conservative: 4  
 Best Local Similarity: 95.0% Mismatches: 0  
 Query Match: 98.0% Indels: 0  
 DB: 6 Gaps: 0

US-09-759-584-59 (1-80) x CD833661 (1-523)

QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaLeuValLeuPheAlaAla 20  
 |||||  
 Db 52 ATGGCTAAGTTTGCTTCCATGCTGTCCTCTCTTCTGCGCTTGTATTATTGCTGCT 111  
 |||||

QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40  
 |||||  
 Db 112 TTCGAAGCACCACCAATGCTGGAAGCACAGAAGCTGTGCGAAGGCCAAGTGGACGTGG 171  
 |||||

QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAArgLeuGluLysAla 60  
 |||||  
 Db 172 TCAGGAGTCTGTGGAACAATAATGTCATGCAAGATCAGTGCATTCGACTAGAGAAGCA 231  
 |||||

QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
 |||||  
 Db 232 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAAGTGCATCTGCTACTTCCCTTGT 291  
 |||||

RESULT 5  
 CD828840

LOCUS  
 DEFINITION  
 CD828840 543 bp mRNA linear EST 10-JUL-2003  
 BN40.040A23F011019 BN40 Brassica napus cDNA clone BN40040A23, mRNA  
 sequence.  
 ACCESSION  
 CD828840  
 VERSION  
 CD828840.1 GI:32510780  
 EST.  
 SOURCE  
 Brassica napus (rape)  
 ORGANISM  
 Brassica napus  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE  
 1 (bases 1 to 543)  
 Genoplatne.  
 AUTHORS  
 Genoplatne, a major partnership french program in plant genomics  
 TITLE  
 Unpublished (2003)  
 JOURNAL  
 COMMENT  
 Contact: Genoplatne  
 Genoplatne  
 93, rue Henri Rochefort 91025 EVRY CEDEX France  
 Tel: 33 1 69 47 54 00  
 Fax: 33 1 69 47 54 10  
 This sequence has been generated in the framework of the french  
 plant genomics programme 'Genoplatne' (<http://www.genoplatne.com>  
 and <http://genoplatne-info.infobiogen.fr>).

FEATURES  
 source  
 1..543  
 Location/Qualifiers  
 /organism="Brassica napus"  
 /mol\_type="mRNA"  
 /cultivar="Jet Neuf"  
 /db\_xref="taxon:3708"  
 /clone="BN40040A23"  
 /tissue\_type="seed"  
 /clone\_lib="BN40"

ORIGIN  
 Alignment Scores:  
 Pred. No.: 1.57e-40 Length: 543  
 Score: 432.00 Matches: 76  
 Percent Similarity: 100.0% Conservative: 4  
 Best Local Similarity: 95.0% Mismatches: 0  
 Query Match: 98.0% Indels: 0  
 DB: 6 Gaps: 0

US-09-759-584-59 (1-80) x CD828840 (1-543)

QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20  
 |||||  
 Db 51 ATGGCTAAGTTTGCTTCCATGCTGTCCTCTCTTCTGCGCTTGTATTATTGCTGCT 110  
 |||||

QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40  
 |||||  
 Db 111 TTCGAAGCACCACCAATGCTGGAAGCACAGAAGCTGTGCGAAGGCCAAGTGGACGTGG 170  
 |||||

QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAArgLeuGluLysAla 60  
 |||||  
 Db 171 TCAGGAGTCTGTGGAACAATAATGTCATGCAAGATCAGTGCATTCGACTAGAGAAGCA 230  
 |||||

QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
 |||||  
 Db 231 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAAGTGCATCTGCTACTTCCCTTGT 290  
 |||||

RESULT 6  
 CD833938  
 LOCUS  
 DEFINITION  
 BN45.040A23F011018 BN45 Brassica napus cDNA clone BN45040A23, mRNA  
 sequence.  
 ACCESSION  
 CD833938  
 VERSION  
 CD833938.1 GI:32515878  
 EST.  
 SOURCE  
 Brassica napus (rape)  
 ORGANISM  
 Brassica napus  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 522)  
 AUTHORS Genoplante, a major partnership french program in plant genomics  
 TITLE Unpublished (2003)  
 JOURNAL  
 COMMENT  
 Genoplante  
 93, rue Henri Rochefort 91025 EVRY CEDEX France  
 Tel: 33 1 69 47 54 00  
 Fax: 33 1 69 47 54 10  
 This sequence has been generated in the framework of the french  
 plant genomics programme 'Genoplante' (<http://www.genoplante.com>  
 and <http://genoplante-info.infobiogen.fr>).

## FEATURES

source

Location/Qualifiers  
 1..522  
 /organism="Brassica napus"  
 /mol\_type="mRNA"  
 /cultivar="Jet Neuf"  
 /db\_xref="taxon:3708"  
 /clone="BN45040A23"  
 /issue\_type="seed"  
 /clone\_lib="BN45"

## ORIGIN

Alignment Scores:  
 Pred. No.: 4,42e-40 Length: 522  
 Score: 428.00 Matches: 75  
 Percent Similarity: 100.0% Conservative: 5  
 Best Local Similarity: 93.8% Mismatches: 0  
 Query Match: 97.1% Indels: 0  
 DB: 6 Gaps: 0

US-09-759-584-59 (1-80) x CD833938 (1-522)

QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20  
 |||||  
 Db 51 ATGGCTAAGTTGCTTCCATCGTTGCCCTCTTTCTCTGCCCCTGTTATTTTGTGCT 110  
 |||||  
 QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTTP 40  
 |||||  
 Db 111 TTGGAAGCACCACAAATGTTGGGAAGCACAGAACTGTGCGAAGGCCAAGTGGACGTGG 170  
 |||||  
 QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60  
 |||||  
 Db 171 TCAGGAGTCTGTGGAAACAAATATGATGATCAAGATCAGTGCATTCGATCAAGAAAGCA 230  
 |||||  
 QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
 |||||  
 Db 231 CGACATGGATCTTGCACATATGTTCCAGCTCACAAGTGCACTGCTACTTCCCTTGT 290  
 |||||

RESULT 7  
 CD829429  
 LOCUS BN40.042806F011226 BN40 Brassica napus cDNA clone BN40042B06, mRNA  
 DEFINITION sequence.  
 ACCESSION CD829429  
 VERSION CD829429.1 GI:32511369  
 KEYWORDS EST.  
 SOURCE Brassica napus (rape)  
 ORGANISM  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 646)  
 AUTHORS Genoplante.  
 TITLE Genoplante, a major partnership french program in plant genomics  
 JOURNAL Unpublished (2003)  
 COMMENT  
 Genoplante  
 93, rue Henri Rochefort 91025 EVRY CEDEX France  
 Tel: 33 1 69 47 54 00  
 Fax: 33 1 69 47 54 10  
 This sequence has been generated in the framework of the french  
 plant genomics programme 'Genoplante' (<http://www.genoplante.com>  
 and <http://genoplante-info.infobiogen.fr>).

and <http://genoplante-info.infobiogen.fr>.

## FEATURES

source

Location/Qualifiers  
 1..646  
 /organism="Brassica napus"  
 /mol\_type="mRNA"  
 /cultivar="Jet Neuf"  
 /db\_xref="taxon:3708"  
 /clone="BN40042B06"  
 /issue\_type="seed"  
 /clone\_lib="BN40"

## ORIGIN

Alignment Scores:  
 Pred. No.: 5,85e-40 Length: 646  
 Score: 428.00 Matches: 75  
 Percent Similarity: 98.8% Conservative: 4  
 Best Local Similarity: 93.8% Mismatches: 1  
 Query Match: 97.1% Indels: 0  
 DB: 6 Gaps: 0

US-09-759-584-59 (1-80) x CD829429 (1-646)

QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20  
 |||||  
 Db 45 ATGGCTAAGTTGCTTCCATCGTTGCCCTCTTTCTCTGCCCCTGTTATTTTGTGCT 104  
 |||||  
 QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTTP 40  
 |||||  
 Db 105 TTGGAAGCACCACAAATGTTGGGAAGCACAGAACTGTGCGAAGGCCAAGTGGACGTGG 164  
 |||||  
 QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60  
 |||||  
 Db 165 TCAGGAGTCTGTGGAAACAAATATGATGATCAAGATCAGTGCATTCGATCAAGAAAGCA 224  
 |||||  
 QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
 |||||  
 Db 225 CGGATGATGATCTTGCACATATGTTCCAGCTCACAAGTGCACTGCTACTTCCCTTGT 284  
 |||||

## RESULT 8

CN826227

LOCUS

DEFINITION

EL1386 Brassica embryo library (EL) Brassica napus cDNA clone

EL1386 complete, mRNA sequence.

ACCESSION

CN826227

VERSION

CN826227.1 GI:65296011

KEYWORDS

EST.

SOURCE

Brassica napus (rape)

ORGANISM

Brassica napus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE

AUTHORS

TITLE

Brassica napus ESTs

JOURNAL

Unpublished (2004)

COMMENT

Contact: Sharpe, A.G.  
 Molecular Genetics  
 Agriculture & Agri-Food Canada  
 107 Science Place, Saskatoon, Saskatchewan, Canada, S7N0X2  
 Tel: 306 956 7271  
 Fax: 306 956 7247  
 Email: [sharpea@agr.gc.ca](mailto:sharpea@agr.gc.ca)  
 Seq primer: M13 Forward and T7.  
 Location/Qualifiers  
 1..413  
 /organism="Brassica napus"  
 /mol\_type="mRNA"  
 /cultivar="DH12075 (double haploid line from Cresor x  
 Westar cross)"  
 /db\_xref="taxon:3708"  
 /clone="EL1386"  
 /dev\_stage="Mid to late embryos (4-6 mg)"  
 /lab\_host="E. coli Electromax DH5 alpha-e (Invitrogen)"

/clone lib="Brassica embryo library (EL)"  
 /notes="Organ: Embryos without seed coat; Vector: pSPOR1  
 (modified: GCGCCGCC\*GACTAGTACCTC\*cgacgcgtggTCGAC);  
 Site 1: Noti; Site 2: Sali; Seeds were collected by Dr.  
 Francois Ouellet when they were still very green (mid to  
 large stage, cotyledons were formed). The seed coats were  
 removed and the remaining tissue was used for cDNA library  
 construction. mRNA was poly-A primed using Superscript  
 Plasmid System cDNA Synthesis and Cloning kit (Invitrogen)  
 After initial screening, the most abundant redundant  
 clones were screened out using 22 oligos designed to match  
 napins (including albumins), cruciferins, oleosins, HSP70,  
 trypsin inhibitor 2, cytosolic GAPDH, cyclophilins, HSP70,  
 desaturase, and CAB (LHCP)."

## ORIGIN

Alignment Scores:  
 Pred. No.: 4.26e-40 Length: 413  
 Score: 427.00 Matches: 77  
 Percent Similarity: 97.5% Conservative: 1  
 Best Local Similarity: 96.2% Mismatches: 2  
 Query Match: 96.8% Indels: 0  
 DB: 7 Gaps: 0

US-09-759-584-59 (1-80) x CN826227 (1-413)

QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaLeuValLeuPheAlaA 20  
 |||||  
 Db 28 ATGGCTAAGTTGCTTCCATCATTTGCTTCTTTTGTCTCTTTTGTCTGCT 87  
 |||||  
 QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTyr 40  
 |||||  
 Db 88 CTCGAAGCACCACCAATGCTGGAAGCACAGAAGTTGTGCGAGAGGCCAAGTGGGACATGG 147  
 |||||  
 QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60  
 |||||  
 Db 148 TCAGAGTCTGTGGAACAACATTAACGATCGAAGATCAGTGCATTAAACCTTGAGAAGCA 207  
 |||||  
 QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
 |||||  
 Db 208 CGACATGGATCTTGCACATATGCTTCCAGCTCACAAGTGATTTGCTACTTCCCTTGT 267  
 |||||

## RESULT 9

CD832625  
 LOCUS BN40.064A14F011227 BN40 Brassica napus cDNA clone BN40064A14, mRNA  
 DEFINITION  
 sequence.  
 ACCESSION CD832625  
 VERSION CD832625.1 GI:32514565  
 KEYWORDS EST.  
 SOURCE Brassica napus (rape)  
 ORGANISM Brassica napus  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

## REFERENCE

AUTHORS Genoplante.  
 TITLE Genoplante, a major partnership french program in plant genomics  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Genoplante  
 Genoplante  
 93, rue Henri Rochefort 91025 EVRY CEDEX France  
 Tel: 33 1 69 47 54 00  
 Fax: 33 1 69 47 54 10  
 This sequence has been generated in the framework of the french  
 plant genomics programme 'Genoplante' (http://www.genoplante.com  
 and http://genoplante-info.infobiogen.fr).

## FEATURES

source  
 1..418  
 /organism="Brassica napus"  
 /mol\_type="mRNA"  
 /cultivar="Jet Neuf"  
 /db\_xref="taxon:3708"

/clone="BN40064A14"  
 /tissue\_type="seed"  
 /clone\_lib="BN40"

## ORIGIN

Alignment Scores:  
 Pred. No.: 4.33e-40 Length: 418  
 Score: 427.00 Matches: 77  
 Percent Similarity: 97.5% Conservative: 1  
 Best Local Similarity: 96.2% Mismatches: 2  
 Query Match: 96.8% Indels: 0  
 DB: 6 Gaps: 0

US-09-759-584-59 (1-80) x CD832625 (1-418)

QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaLeuValLeuPheAlaA 20  
 |||||  
 Db 53 ATGGCAAGTTGCTTCCATCATTTGCTTCTTTTGTCTCTTTTGTCTGCT 112  
 |||||  
 QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTyr 40  
 |||||  
 Db 113 CTCGAAGCACCACCAATGCTGGAAGCACAGAAGTTGTGCGAGAGGCCAAGTGGGACATGG 172  
 |||||  
 QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60  
 |||||  
 Db 173 TCAGAGTCTGTGGAACAACATTAACGATCGAAGATCAGTGCATTAAACCTTGAGAAGCA 232  
 |||||  
 QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
 |||||  
 Db 233 CGACATGGATCTTGCACATATGCTTCCAGCTCACAAGTGATTTGCTACTTCCCTTGT 292  
 |||||

## RESULT 10

CD833944  
 LOCUS BN45.040B07F011019 BN45 Brassica napus cDNA clone BN45040B07, mRNA  
 DEFINITION  
 sequence.  
 ACCESSION CD833944  
 VERSION CD833944.1 GI:32515884  
 KEYWORDS EST.  
 SOURCE Brassica napus (rape)  
 ORGANISM Brassica napus  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

## REFERENCE

AUTHORS Genoplante.  
 TITLE Genoplante, a major partnership french program in plant genomics  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Genoplante  
 Genoplante  
 93, rue Henri Rochefort 91025 EVRY CEDEX France  
 Tel: 33 1 69 47 54 00  
 Fax: 33 1 69 47 54 10  
 This sequence has been generated in the framework of the french  
 plant genomics programme 'Genoplante' (http://www.genoplante.com  
 and http://genoplante-info.infobiogen.fr).

## FEATURES

source  
 1..420  
 /organism="Brassica napus"  
 /mol\_type="mRNA"  
 /cultivar="Jet Neuf"  
 /db\_xref="taxon:3708"  
 /clone="BN45040B07"  
 /tissue\_type="seed"  
 /clone\_lib="BN45"

## ORIGIN

Alignment Scores:  
 Pred. No.: 4.36e-40 Length: 420  
 Score: 427.00 Matches: 77  
 Percent Similarity: 97.5% Conservative: 1  
 Best Local Similarity: 96.2% Mismatches: 2  
 Query Match: 96.8% Indels: 0



```
LOCUS
DEFINITION CD833977 421 bp mRNA linear EST 10-JUL-2003
            BN45.040D05F011019 BN45 Brassica napus cDNA clone BN45040D05, mRNA
            sequence.
ACCESSION  CD833977
VERSION    CD833977.1 GI:32515917
KEYWORDS   EST.
ORGANISM   Brassica napus (rape)
SOURCE     Brassica napus
REFERENCE  1 (bases 1 to 421)
AUTHORS   Genoplante.
TITLE     Genoplante, a major partnership french program in plant genomics
JOURNAL   Unpublished (2003)
COMMENT   Contact: Genoplante
          93, rue Henri Rochefort 91025 EVRY CEDEX France
          Tel: 33 1 69 47 54 00
          Fax: 33 1 69 47 54 10
          This sequence has been generated in the framework of the french
          plant genomics programme 'Genoplante' (http://www.genoplante.com)
          and http://genoplante-info.infobiogen.fr.

FEATURES             source
source               1..421
                     /organism="Brassica napus"
                     /mol_type="mRNA"
                     /cultivar="Jet Neuf"
                     /db_xref="taxon:3708"
                     /clone="BN45040D05"
                     /tissue_type="seed"
                     /clone_lib="BN45"

ORIGIN
Alignment Scores:  4.37e-40  Length: 421
Pred. No.:        427.00    Matches: 77
Score:            97.5%     Conservative: 1
Percent Similarity: 96.2%   Mismatches: 2
Best Local Similarity: 96.2% Indels: 0
Query Match:      96.8%    Gaps: 0
DB:
US-09-759-584-59 (1-80) x CD833977 (1-421)

QY 1 MetAlaLysPheAlaSerIleIleAlaLeuPheAlaAlaLeuValLeuPheAlaAla 20
   |||||
Db 51 ATGGCTAAGTTGCTTCCATCATGTCCTACTTTTGGCTGCTTTGCTGCTT 110
   |||||

QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
   |||||
Db 111 CTCGAAGCACCACCAATGTTGGAAGCACAGAAAGTTGTGGAGAGGCCAAGTGGACATGG 170
   |||||

QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
   |||||
Db 171 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGATCAGTGCATTAACCTTGGAAGAAGCA 230
   |||||

QY 61 AtgHisGlySerCysAsnTrpValPheProAlaHisLysCysIleCysTrpPheProCys 80
   |||||
Db 231 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAGTGATTTGCTACTTCCCTTGT 290

RESULT 14
CD833983
LOCUS
DEFINITION CD833983 422 bp mRNA linear EST 10-JUL-2003
            BN45.040D11F011019 BN45 Brassica napus cDNA clone BN45040D11, mRNA
            sequence.
ACCESSION  CD833983
VERSION    CD833983.1 GI:32515923
KEYWORDS   EST.
SOURCE     Brassica napus (rape)
ORGANISM   Brassica napus
REFERENCE  1 (bases 1 to 422)
AUTHORS   Genoplante.
TITLE     Genoplante, a major partnership french program in plant genomics
JOURNAL   Unpublished (2003)
COMMENT   Contact: Genoplante
          93, rue Henri Rochefort 91025 EVRY CEDEX France
          Tel: 33 1 69 47 54 00
          Fax: 33 1 69 47 54 10
          This sequence has been generated in the framework of the french
          plant genomics programme 'Genoplante' (http://www.genoplante.com)
          and http://genoplante-info.infobiogen.fr.

FEATURES             source
source               1..422
                     /organism="Brassica napus"
                     /mol_type="mRNA"
                     /cultivar="Jet Neuf"
                     /db_xref="taxon:3708"
                     /clone="BN45040D11"
                     /tissue_type="seed"
                     /clone_lib="BN45"

ORIGIN
Alignment Scores:  4.39e-40  Length: 422
Pred. No.:        427.00    Matches: 77
Score:            97.5%     Conservative: 1
Percent Similarity: 96.2%   Mismatches: 2
Best Local Similarity: 96.2% Indels: 0
Query Match:      96.8%    Gaps: 0
DB:
US-09-759-584-59 (1-80) x CD833983 (1-422)

QY 1 MetAlaLysPheAlaSerIleIleAlaLeuPheAlaAlaLeuValLeuPheAlaAla 20
   |||||
Db 51 ATGGCTAAGTTGCTTCCATCATGTCCTACTTTTGGCTGCTTTGCTGCTT 110
   |||||

QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
   |||||
Db 111 CTCGAAGCACCACCAATGTTGGAAGCACAGAAAGTTGTGGAGAGGCCAAGTGGACATGG 170
   |||||

QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
   |||||
Db 171 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGATCAGTGCATTAACCTTGGAAGAAGCA 230
   |||||

QY 61 AtgHisGlySerCysAsnTrpValPheProAlaHisLysCysIleCysTrpPheProCys 80
   |||||
Db 231 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAGTGATTTGCTACTTCCCTTGT 290

RESULT 15
CD827413
LOCUS
DEFINITION CD827413 426 bp mRNA linear EST 10-JUL-2003
            BN25.067G02F020123 BN25 Brassica napus cDNA clone BN25067G02, mRNA
            sequence.
ACCESSION  CD827413
VERSION    CD827413.1 GI:32509353
KEYWORDS   EST.
SOURCE     Brassica napus (rape)
ORGANISM   Brassica napus
REFERENCE  1 (bases 1 to 426)
AUTHORS   Genoplante.
TITLE     Genoplante, a major partnership french program in plant genomics
JOURNAL   Unpublished (2003)
COMMENT   Contact: Genoplante
          93, rue Henri Rochefort 91025 EVRY CEDEX France
          Tel: 33 1 69 47 54 00
          Fax: 33 1 69 47 54 10
          This sequence has been generated in the framework of the french
          plant genomics programme 'Genoplante' (http://www.genoplante.com)
          and http://www.genoplante.com
```

and <http://genoplante-info.infobiogen.fr>.

FEATURES  
source  
1. .426  
Location/Qualifiers  
/organism="Brassica napus"  
/mol\_type="mRNA"  
/cultivar="Jet Neuf"  
/db\_xref="taxon:3708"  
/clone="BN25067G02"  
/tissue\_type="seed"  
/clone\_lib="BN25"

ORIGIN

Alignment Scores:  
Pred. No.: 4,44e-40 Length: 426  
Score: 427.00 Matches: 77  
Percent Similarity: 97.5% Conservative: 1  
Best Local Similarity: 96.2% Mismatches: 2  
Query Match: 96.8% Indels: 0  
DB: 6 Gaps: 0

US-09-759-584-59 (1-80) x CD827413 (1-426)

QY	1	MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla	20
DB	51	ATGGCTAAGTTTGCTTCCATCATTTGCTGCTCTTTGCTGCTCTTTGCTGCT	110
QY	21	PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp	40
DB	111	CTCGAAGCACCAACAATGGTGAAGCACAGAGTTGTGCGAGAGGCCAAGTGGGACATGG	170
QY	41	SerGlyValCysGlyAsnAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla	60
DB	171	TCAGGAGTCTGTGGAAACATAACGCAATGCAAGATCAGTGCATTAACCTTGGAAGCA	230
QY	61	ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys	80
DB	231	CGACATGGATCTTGGCAACTATGTCCTCCAGCTCACAAAGTGATTTTGTACTTCCCTGT	290

Search completed: May 10, 2006, 09:42:56  
Job time : 3006.5 secs

GenCore version 5.1.1.8  
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OM protein - nucleic search, using frame plus p2n model

Run on: May 10, 2006, 05:46:44 ; Search time 3626 Seconds  
(without alignments)  
1881.195 Million cell updates/sec

Title: US-09-759-584-49  
Perfect score: 442  
Sequence: 1 MAKFSIALLPALVFAA.....RHGSCNYVPPAHKICYPFC 80

Scoring table:  
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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delopt 6.0 , Delopt 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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- 2: gb.in.\*
- 3: gb.env.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pr.\*
- 9: gb.ro.\*
- 10: gb.sts.\*
- 11: gb.sv.\*
- 12: gb.un.\*
- 13: gb.vi.\*
- 14: gb.htg.\*
- 15: gb.pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	442	100.0	285	6	AR014692 Sequence
2	442	100.0	285	6	AR432392 Sequence
3	442	100.0	395	15	RSU18557 Raphanus sa

4	442	100.0	414	6	A26875	A26875 R.sativus A
5	442	100.0	414	6	A39549	A39549 Sequence 37
6	442	100.0	414	6	A63404	A63404 Sequence 19
7	442	100.0	414	6	AR050153	AR050153 Sequence
8	442	100.0	414	6	AR130272	AR130272 Sequence
9	442	100.0	414	6	I23728	I23728 Sequence 48
10	442	100.0	414	6	AR207337	AR207337 Sequence
11	442	100.0	414	6	AR374914	AR374914 Sequence
12	442	100.0	414	6	AR642703	AR642703 Sequence
13	433	98.0	285	6	AR014693	AR014693 Sequence
14	433	98.0	285	6	AR432393	AR432393 Sequence
15	433	98.0	288	6	A39553	A39553 Sequence 41
16	433	98.0	288	6	AR050161	AR050161 Sequence
17	433	98.0	288	6	AR130280	AR130280 Sequence
18	433	98.0	288	6	I23736	I23736 Sequence 58
19	423	95.7	449	6	E34290	E34290 Phage and p
20	418	94.6	575	6	BD223249	BD223249 Method of
21	417	94.3	457	15	RSU18556	U18556 Raphanus sa
22	414	93.7	243	15	AY998243	AY998243 Sinapis a
23	407	92.1	243	6	BD174927	BD174927 Disease t
24	407	92.1	414	6	E31545	E31545 Antibacteri
25	407	92.1	414	15	AB012871	AB012871 Wasabia j
26	405	91.6	499	15	RSAP94	X97318 R.sativus m
27	403	91.2	243	6	AX412329	AX412329 Sequence
28	403	91.2	243	6	AX412502	AX412502 Sequence
29	403	91.2	243	6	AX507351	AX507351 Sequence
30	403	91.2	243	6	AX590057	AX590057 Sequence
31	403	91.2	274	15	AY133787	AY133787 Arabidops
32	403	91.2	400	6	A68647	A68647 Sequence 15
33	403	91.2	454	15	AY063779	AY063779 Arabidops
34	402	91.0	243	6	BD174928	BD174928 Disease t
35	402	91.0	363	15	AF528180	AF528180 Brassica
36	402	91.0	416	6	E31546	E31546 Antibacteri
37	402	91.0	416	15	AB012872	AB012872 Eutrema w
38	397	89.8	243	6	AX412406	AX412406 Sequence
39	397	89.8	243	6	AX412601	AX412601 Sequence
40	397	89.8	243	6	AX651878	AX651878 Sequence
41	397	89.8	243	15	AY060506	AY060506 Arabidops
42	397	89.8	403	6	A68645	A68645 Sequence 13
43	397	89.8	403	15	ATANTSPEC	X91916 A.thaliana
44	397	89.8	425	15	AY052236	AY052236 Arabidops
45	396.5	89.7	270	6	AR014691	AR014691 Sequence

ALIGNMENTS

RESULT 1	AR014692	Sequence 16 from patent US 5773696.	285 bp	DNA	linear	PAT 05-DEC-1998
LOCUS	AR014692					
DEFINITION	AR014692					
ACCESSION	AR014692					
VERSION	AR014692.1	GI:3972146				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 285)					
AUTHORS	Liang,J., Shah,D,Maganlal., Wu,Y,Shun, and Rosenberger,C Annette.					
TITLE	Antifungal polypeptide and methods for controlling plant pathogenic fungi					
JOURNAL	Patent: US 5773696-A 16 30-JUN-1998;					
FEATURES	Location/Qualifiers					
source	1..285					
	/organism="unknown"					
	/mol_type="unassigned DNA"					
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Score:	442.00	Matches:	80			
Percent Similarity:	100.0%	Conservative:	0			
Best Local Similarity:	100.0%	Mismatches:	0			
Query Match:	100.0%	Indels:	0			

DB:	6	Gaps:	0
US-09-759-584-49 (1-80) x AR014692 (1-285)			
Qy	1	MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla	20
Db	31	ATGGCTAAGTTTGGCGCCATCATCGACCTCTTTGCTGCTCTCTTTGCTGCT	90
Qy	21	PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp	40
Db	91	TTTCAGGACCAACATATGTTGGAGGCACAAAGATTGTCGAGAGCCATCAGGACTGG	150
Qy	41	SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla	60
Db	151	TCAGGAGTCTGGGAAACAACAACGCATCGCAAGAACCAATGCATCAACTCGAGAGGCA	210
Qy	61	ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys	80
Db	211	CGGCATGGATCTTGGCAATACGCTTCCAGCTCAAGATGCATCTGCTACTTTCCATGC	270
RESULT 2			
LOCUS	AR432392	285 bp	DNA linear PAT 18-DEC-2003
DEFINITION	Sequence 16 from patent US 6653280.		
ACCESSION	AR432392		
VERSION	AR432392.1 GI:40194669		
KEYWORDS	Unknown.		
SOURCE	ORGANISM		
REFERENCE	1 (bases 1 to 285)		
AUTHORS	Liang, J., Shah, D.M., Wu, Y.S. and Rosenberger, C.A.		
TITLE	Antifungal polypeptide AlyAPP from Alyssum and methods for controlling plant pathogenic fungi		
JOURNAL	Patent: US 6653280-A 16 25-NOV-2003;		
FEATURES	Monsanto Technology LLC; St. Louis, MO		
source	1. .285		
ORIGIN	/organism="unknown"		
Alignment Scores:	/mol_type="genomic DNA"		
Pred. No.:	7.09e-45	Length:	285
Score:	442.00	Matches:	80
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	6	Gaps:	0
US-09-759-584-49 (1-80) x AR432392 (1-285)			
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Db	31	ATGGCTAAGTTTGGCGCCATCATCGACCTCTTTGCTGCTCTCTTTGCTGCT	90
Qy	21	PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp	40
Db	91	TTTCAGGACCAACATATGTTGGAGGCACAAAGATTGTCGAGAGCCATCAGGACTGG	150
Qy	41	SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla	60
Db	151	TCAGGAGTCTGGGAAACAACAACGCATCGCAAGAACCAATGCATCAACTCGAGAGGCA	210
Qy	61	ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys	80
Db	211	CGGCATGGATCTTGGCAATACGCTTCCAGCTCAAGATGCATCTGCTACTTTCCATGC	270
RESULT 3			
LOCUS	RSU18557	395 bp	mRNA linear PLN 07-JUL-1995
DEFINITION	Raphanus sativus antifungal protein 1 preprotein (Rs-AfPi) mRNA, complete cds.		

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Db      75  TTGGAAGCACCACCAATGTGTGAAGCACAAGAAGTTGTGGAAGGCCAAGTGGGACATGG 134
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Qy      41  SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
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Db      135 TCAGGAGTCTGTGGAACCAATAACGATCGATCAAGATCACTGATTAACCTTGGAAGAACA 194
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Qy      61  ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
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Db      195 CGACATGGATCTTGGAACTATGTCTTCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 254

RESULT 4
A26875
LOCUS      A26875                      414 bp    DNA        linear    PAT 30-NOV-2001
DEFINITION R.sativus AFP1 gene.
ACCESSION  A26875
VERSION    A26875.1  GI:1247352
KEYWORDS
SOURCE    Raphanus sativus (radish)
ORGANISM  Raphanus sativus
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
           rosids; eurosids II; Brassicales; Brassicaceae; Raphanus.
REFERENCE  1 (bases 1 to 414)
AUTHORS   Broekaert,W.F., Cammue,B.P.A., Terras,F.R.G., Vanderleyden,J.,
           Osborn,R.W. and Rees,S.B.
TITLE     BIOCIDAL PROTEINS
JOURNAL   Patent: WO 9305153-A 33 18-MAR-1993;
           ICI PLC (GB)
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Query Match:    100.0%      Indels:      0
Db:             6      Gaps:      0

US-09-759-584-49 (1-80) x A26875 (1-414)

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Db      16  ATGGCTAAGTTTGGCTCCATCATCGCACTCTTTTGTGCTCTTTGCTCTTTTCTGCTGT 75
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Qy      21  PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
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Db      76  TTCGAAGCACCAACAATGTGTGAAGCACAAGAAGTTGTGGAAGGCCAAGTGGGACATGG 135
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Qy      41  SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
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Db      136 TCAGGAGTCTGTGGAACCAATAACGATCGATCAAGATCACTGATTAACCTTGGAAGAACA 195
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Qy      61  ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
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Db      196 CGACATGGATCTTGGAACTATGTCTTCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255

RESULT 5
A39549
LOCUS      A39549                      414 bp    DNA        linear    PAT 05-MAR-1997
DEFINITION Sequence 37 from Patent WO9416076.
ACCESSION  A39549
VERSION    A39549.1  GI:2295842
KEYWORDS
SOURCE    unidentified
ORGANISM  unidentified
           unclassified sequences.
REFERENCE  1 (bases 1 to 414)

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AUTHORS   Dubock,A.C., Powell,K.A. and Rees,S.B.
TITLE     ANTIMICROBIAL-PROTEIN-PRODUCING ENDOSYMBIOTIC MICROORGANISMS
JOURNAL   Patent: WO 9416076-A 37 21-JUL-1994;
           ZENECA LTD (GB)
COMMENT   Other publication AU 5820494 940815.
FEATURES
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Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match:    100.0%      Indels:      0
Db:             6      Gaps:      0

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Qy      21  PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
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Db      76  TTCGAAGCACCAACAATGTGTGAAGCACAAGAAGTTGTGGAAGGCCAAGTGGGACATGG 135
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Qy      41  SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
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Db      136 TCAGGAGTCTGTGGAACCAATAACGATCGATCAAGATCACTGATTAACCTTGGAAGAACA 195
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Qy      61  ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
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Db      196 CGACATGGATCTTGGCACTATGTCTTCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255

RESULT 6
A63404
LOCUS      A63404                      414 bp    DNA        linear    PAT 12-MAR-1998
DEFINITION Sequence 19 from Patent WO9721814.
ACCESSION  A63404
VERSION    A63404.1  GI:3717176
KEYWORDS
SOURCE    unidentified
ORGANISM  unidentified
           unclassified sequences.
REFERENCE  1
AUTHORS   Broekaert,W.F., De,S.G., Rees and Sarah,B.
TITLE     ANTIFUNGAL PROTEINS
JOURNAL   Patent: WO 9721814-A 19 19-JUN-1997;
           ZENECA LTD (GB)
COMMENT   Other publication AU 1105397 19970703.
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Query Match:    100.0%      Indels:      0
Db:             6      Gaps:      0

US-09-759-584-49 (1-80) x A63404 (1-414)

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Qy 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTTP 40  
Db 76 TTCGAAGCACCACCAATGTTGGGAAGCACAAGAAGTTGTGCGAAAGGCCAAAGTGGGACATGG 135  
Qy 41 SerGlyValCysGlyAsnAenAenAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60  
Db 136 TCAGGAGTCTGTGGAAACCAATACCGATCGCAAGATCAGTGCATTAACTTGAAGAAGCA 195  
Qy 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
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LOCUS 123728 414 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 48 from patent US 5824869.  
ACCESSION AR050153  
VERSION AR050153.1 GI:5972145  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 414)  
AUTHORS Broekaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B.,  
Terras, F.R.G. and Vanderleyden, J.  
TITLE Biocidal proteins  
JOURNAL Patent: US 5824869-A 48 20-OCT-1998;  
FEATURES Location/Qualifiers  
source 1. .414  
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Query Match: 100.0% Indels: 0  
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Qy 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTTP 40  
Db 76 TTCGAAGCACCACCAATGTTGGGAAGCACAAGAAGTTGTGCGAAAGGCCAAAGTGGGACATGG 135  
Qy 41 SerGlyValCysGlyAsnAenAenAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60  
Db 136 TCAGGAGTCTGTGGAAACCAATACCGATCGCAAGATCAGTGCATTAACTTGAAGAAGCA 195  
Qy 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
Db 196 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAAGTGATCTGCTACTTTCCTTGT 255  
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LOCUS 123728 414 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 48 from patent US 6187904.  
ACCESSION AR130272  
VERSION AR130272.1 GI:14118169  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 414)  
AUTHORS Broekaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B.,

Terras, F.R.G. and Vanderleyden, J.  
Biocidal proteins  
Patent: US 6187904-A 48 13-FEB-2001;  
Location/Qualifiers  
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Alignment Scores: 1.08e-44 Length: 414  
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Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
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Db 16 ATGGCTAAGTTGGCGTCCATCATCGCACCTCTCTTTTGGCTGCTCTGTTCTTTTGGCTGCT 75  
Qy 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTTP 40  
Db 76 TTCGAAGCACCACCAATGTTGGGAAGCACAAGAAGTTGTGCGAAAGGCCAAAGTGGGACATGG 135  
Qy 41 SerGlyValCysGlyAsnAenAenAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60  
Db 136 TCAGGAGTCTGTGGAAACCAATACCGATCGCAAGATCAGTGCATTAACTTGAAGAAGCA 195  
Qy 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
Db 196 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAAGTGATCTGCTACTTTCCTTGT 255  
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LOCUS 123728  
DEFINITION Sequence 48 from patent US 5538525.  
ACCESSION I23728  
VERSION I23728.1 GI:1603598  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 414)  
AUTHORS Broekaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B.,  
Terras, F.R.G. and Vanderleyden, J.  
TITLE Biocidal proteins  
JOURNAL Patent: US 5538525-A 48 23-JUL-1996;  
FEATURES Location/Qualifiers  
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QY	61	ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys	80
Db	196	CGACATGGATCTTGGCAACTATGTCTTCCAGCTCACAAGTGATCTGCTACTTTCCTTGT	255
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DEFINITION	Sequence 17 from patent US 5773696.		
ACCESSION	AR014693		
VERSION	AR014693.1	GI:3972147	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 285)		
AUTHORS	Liang,J., Shah,D.Maganlal., Wu,Y.Shun. and Rosenberger,C.Annette.		
TITLE	Antifungal polypeptide and methods for controlling plant pathogenic fungi		
JOURNAL	Patent: US 5773696-A 17 30-JUN-1998;		
FEATURES	Location/Qualifiers		
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Query Match:	98.0%	Indels:	0
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QY	1	MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla	20
Db	31	ATGGCTAAGTTTGGCTCCATCATCGCACTCCTCTTTGGCTGCTCTCTCTTCTTGTGCT	90
QY	21	PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrrp	40
Db	91	TTTCGAGGCACCAACTATGTGTGGAGGCACAAAAGTTGTGCCAAAGGCCATCAGGAC	150
QY	41	SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla	60
Db	151	TCAGGAGTCTGCGGAACAACACGATGCAAGAACCAATGCATCAGACTCGAGAAGGCA	210
QY	61	ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys	80
Db	211	CGGCATGGATCTTGCACACTACGTCTTCCAGCTCAAGTGCATCTGCTACTTTCATGC	270
RESULT 15			
A39553			
LOCUS	A39553	288 bp	DNA linear PAT 05-MAR-1997
DEFINITION	Sequence 41 from Patent WO9416076.		
ACCESSION	A39553		
VERSION	A39553.1	GI:2295844	
KEYWORDS	unidentified		
SOURCE	unclassified		
ORGANISM	unclassified sequences.		
REFERENCE	1 (bases 1 to 288)		
AUTHORS	Dubock,A.C., Powell,K.A. and Rees,S.B.		
TITLE	ANTIMICROBIAL-PROTEIN-PRODUCING ENDOSYMBIOTIC MICROORGANISMS		
JOURNAL	Patent: WO 9416076-A 41 21-JUL-1994;		
COMMENT	ZENECA LTD (GB)		
FEATURES	Other publication AU 5820494 940815.		
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Alignment Scores:			
Pred. No.:	9.08e-44	Length:	288
Score:	433.00	Matches:	78
Percent Similarity:	98.8%	Conservative:	1
Best Local Similarity:	97.5%	Mismatches:	1
Query Match:	98.0%	Indels:	0
DB:	6	Gaps:	0
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QY	1	MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla	20
Db	43	ATGGCTAAGTTTGGCTCCATCATCGCACTCTTTTGGCTGCTCTCTTCTTGTGCTGCT	102
QY	21	PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrrp	40
Db	103	TTTCGAGGCACCAACATGTGTGGAGGCACAGAAGTTGTGCCAAAGGCCAAGTGGACATGG	162
QY	41	SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla	60
Db	163	TCAGGAGTCTGTGGAAACAATAACGCATGCAAGATCAGTGCATTAGACTTGAGAAAGCA	222

Qy 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
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Search completed: May 10, 2006, 08:02:44  
Job time : 3627 secs

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GenCore version 5.1.1.8  
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OM protein - nucleic search, using frame\_plus\_p2n model  
Run on: May 10, 2006, 05:44:15 ; Search time 452 Seconds  
(without alignments)  
1769.387 Million cell updates/sec

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Perfect score: 442  
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Searched: 4996997 seqs, 3332346308 residues

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Listing first 45 summaries

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- 4: Geneseqn2001as.\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	442	100.0	414	2	AAQ38650
2	442	100.0	414	2	AAQ70128
3	442	100.0	414	2	AAT72333
4	442	100.0	414	2	AAT68696

5	433	98.0	261	2	AAQ38652
6	433	98.0	288	2	AAQ70130
7	432	97.7	394	10	ADCS1221
8	432	97.7	394	13	ADU71300
9	425	96.2	426	10	ADCS1223
10	425	96.2	426	13	ADU71302
11	423	95.7	449	3	AAAS3190
12	418	94.6	575	3	AAZ99339
13	407	92.1	63	6	ABQ82690
14	407	92.1	414	3	AAZ39123
15	403	91.2	243	6	ABZ14241
16	403	91.2	243	6	ADG87651
17	403	91.2	243	6	ADG87824
18	403	91.2	243	8	ABZ42136
19	403	91.2	400	2	AAV10633
20	403	91.2	400	7	ADZ75091
21	402	91.0	243	6	ABQ82691
22	402	91.0	416	3	AAZ39124
23	397	89.8	243	6	ADG87728
24	397	89.8	243	6	ADG87923
25	397	89.8	243	8	ADA68378
26	397	89.8	403	2	AAV10632
27	396.5	89.7	270	2	AAZ94582
28	396.5	89.7	286	2	AAZ94574
29	396.5	89.7	481	2	AAZ99289
30	395	89.4	308	2	AAZ94577
31	384	86.9	500	2	AAZ94581
32	359	81.2	1973	3	AAZ94581
33	358	81.0	1616	2	AAV10646
34	304	68.8	159	10	ADG32304
35	304	68.8	984	10	ADG32343
36	304	68.8	987	10	ADG32350
37	304	68.8	987	10	ADG32348
38	303	68.6	534	3	AAZ99327
39	301.5	68.2	522	3	AAZ99324
40	301	68.1	485	3	AAZ99333
41	301	68.1	1093	3	AAZ99334
42	300	67.9	534	3	AAZ51396
43	300	67.9	534	3	AAZ99325
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ALIGNMENTS

RESULT 1  
AAQ38650  
ID AAQ38650 standard; DNA; 414 BP.

AC AAQ38650;

DT 25-MAR-2003 (revised)  
DT 07-JUL-1993 (first entry)

DE Rs-APP1 cDNA.

XX Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria; fungicide; bactericide; antibiotic; antifungal; gram positive; plant disease resistance; low toxicity.

XX Raphanus sativus.

XX Key Location/Qualifiers  
FT CDS 16..256  
FT /\*tag= a

XX WO9305153-A1.

XX 18-MAR-1993.

XX 27-AUG-1992; 92WO-GB001570.

XX 29-AUG-1991; 91GB-00018523.



crop protection; plant defensin; bacterial protection; preservative; ss.  
Raphanus sativus.

Key Location/Qualifiers  
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FT /tag= c  
FT /product= "antifungal\_protein\_1"

WO9721815-A2.  
19-JUN-1997.

12-DEC-1996; 96WO-GB003068.  
13-DEC-1995; 95GB-00025455.  
28-MAR-1996; 96GB-00006552.  
(ZENE ) ZENECA LTD.  
Meloan RH, Puijk WC, Schaaper WMM, Sijtsma L, Van Amerongen A;  
Broekaert W, Samblanx GW, Fant F, Borremans FAM, Rees SB;  
Van Gelder WMJ;  
WPI; 1997-332786/30.  
P-PSDB; AAW19280.

Antifungal peptide derived from radish antifungal protein 2 - and related DNA, useful for producing plants with increased fungal resistance and as therapeutic or preservative agent.

Claim 8; Fig 2; 65pp; English.

This cDNA sequence encodes an Raphanus sativus (radish) antifungal protein (Rs-APp1). Analogues of the homologous protein, Rs-APP2 (AAW19281), have also been produced (see AAW19282-92, AAW19294-98, AAW19301-04, AAW19330-34 and AAW1765-834). Plants containing DNA sequences encoding these proteins have improved resistance to fungi. Compositions containing the peptides can be used to control fungi or bacteria in pharmaceutical (e.g. treatment of Candida infections) or preservative purposes (as food additives). In agriculture, the peptide may be used to improve disease resistance or disease tolerance of crops, either pre or post harvest. When applied to plants they may also have curative as well as protective actions. The peptides may also be used to protect plants by introducing them, or a microorganism capable of expressing the peptide into the soil. (Updated on 25-MAR-2003 to correct PI field.)

Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 4,04e-46 Length: 414  
Score: 442.00 Matches: 80  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 2 Gaps: 0

US-09-759-584-49 (1-80) x AAW72333 (1-414)

Qy 1 MetaAlaLysPheAlaSerIleAlaLeuPheAlaLeuValLeuPheAlaAla 20  
Db 16 ATGGCTAAGTTGGTGGTCCATCGCACCTCTTTTGGCTGCTCTTTTGGTCT 75  
Qy 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40  
Db 76 TTCGAGACCAACCAATGTTGGTGGGAAGCACGAAGTTGTGGCAAGGCGCAAGTGGCATGG 135

Qy 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60  
Db 136 TCAGGAGTCTGTGGAACAATAACGATCGCAATCACTAGTCACTTAACCTTGAGAAGCA 195  
Qy 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
Db 196 CGACATGATCTTGCACTATGTCTTCCAGCTCAAGGTATCTGACTTCTCTTGT 255

RESULT 4  
AAT68696  
ID AAT68696 standard; cDNA; 414 BP.  
XX AAT68696;  
XX  
XX 13-DEC-1997 (first entry)  
XX Radish antifungal protein 1 (Rs-APP1) cDNA.  
KW Rs-APP1; radish antifungal protein 1; fungicide; salt tolerance;  
XX preservative; transgenic plant; crop protection.  
OS Raphanus sativus.  
FH Key Location/Qualifiers  
FT CDS 16..258  
FT /tag= a  
FT /transl\_except= (pos:85..87, aa:Glu)  
FT sig\_peptide 16..102  
FT /tag= b  
FT mat\_peptide 103..255  
FT /tag= c  
XX  
XX WO9721814-A1.  
PN  
XX  
XX 19-JUN-1997.  
PD  
XX  
XX 12-DEC-1996; 96WO-GB003065.  
XX  
XX 13-DEC-1995; 95GB-00025474.  
XX (ZENE ) ZENECA LTD.  
XX Broekaert WF, De Samblanx GW, Rees SB;  
XX WPI; 1997-332785/30.  
XX P-PSDB; AAW19617.  
XX New active mutants of radish antifungal protein 2 - used to generate fungus-resistant plants or as therapeutic or preservative agents.  
XX Disclosure; Fig 2; 39pp; English.  
XX  
XX This cDNA clone codes for the preprotein for radish antifungal protein 1 (Rs-APP1) (AAW19617). Novel antifungal proteins are based on Rs-APP1, Rs-APP2 (see AAW19616), Rs-APP3 and Rs-APP4, especially those in which Gly9 is replaced by Arg, Val39 by Arg, Gly9 by Arg, Glu5 by Met and/or Gly16 by Met. Mutants (see AAW26371-90) of Rs-APP2 are specifically claimed. The mutants show improved salt tolerant antifungal activity, particularly when expressed in plants

Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 4,04e-46 Length: 414  
Score: 442.00 Matches: 80  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 2 Gaps: 0

US-09-759-584-49 (1-80) x AAT68696 (1-414)

Qy 1 MetaAlaLysPheAlaSerIleAlaLeuPheAlaAlaLeuValLeuPheAlaAla 20

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Db 16 ATGGCTAAGTTGGTCCATCGACATCTTTTGGCTGCTGCTGCTGCT 75
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
Db 76 TTCGAAGCACCACCAATGTTGGGAAGCACAGAAAGTTGTGGAAAGGCGCAAGTGGGACATGG 135
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysAlaAsnLeuGluLysAla 60
Db 136 TCAGGAGTCTGTGGAAACAATACGCATGCAAGATCAGTGCAATTAACCTTGAGAAAGCA 195
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysAlaCysTyrPheProCys 80
Db 196 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAAAGTGTATCTGCTACTTTCCTTCT 255

RESULT 5
AAQ38652
ID AAQ38652 standard; DNA; 261 BP.
XX
AC AAQ38652;
XX
DT 25-MAR-2003 (revised)
DT 07-JUL-1993 (first entry)
XX
DE RS-AFP2 cDNA.
XX
KW Raphanus sativus; Brassica; Arabidopsis; Chnicus; Lathyrus; Clitoria;
KW fungicide; bactericide; antibiotic; antifungal; gram positive;
KW plant disease resistance; low toxicity.
XX
OS Raphanus sativus.
XX
FH Key Location/Qualifiers
FT CDS 16..256
FT /*tag= a
XX
PN WO9305153-A1.
XX
PD 18-MAR-1993.
XX
PF 27-AUG-1992; 92WO-GB001570.
XX
PR 29-AUG-1991; 91GB-00018523.
PR 13-FEB-1992; 92GB-0003038.
PR 25-JUN-1992; 92GB-00013526.
XX
PA (ICIL ) IMPERIAL CHEM IND PLC.
XX
XX Broekaert WF, Cammue BPA, Osborn RW, Rees SB, Terras FRG;
PI Vanderleyden J;
XX
DR WPI; 1993-100978/12.
XX
XX Biocidal proteins isolated from seeds of plants - e.g. brassica or
XX dahlia, useful for increasing plants' resistance to fungal and bacterial
XX diseases.
XX
XX Example 21; Fig 35; 110pp; English.
XX
XX This cDNA represents the sequence of Rs-AFP2 from Raphanus sativus. PCR
XX primer AAQ38640 was used together with AAQ38641 to generate a probe for
XX screening a Raphanus sativus seed cDNA library. This primer corresponds
XX to amino acids 2 to 7 of Rs-AFP1 and has a sense orientation. The 144bp
XX product was partially re-amplified using AAQ38642 and AAQ38641 to give a
XX 123bp product, which was further reamplified with the same primers and
XX digoxigenin-11-dUTP instead of dTTP to give a digoxigenin labeled PCR
XX product. This was used to screen a lambda ZAPII cDNA library by in situ
XX plaque hybridisation. Positive plaques were purified and subjected to two
XX additional screening rounds with the same probe. Inserts were excised in
XX vivo into the pBluescript phagemid form with the aid of helper phage
XX R408. Inserts from 22 positive clones were excised by EcoRI digestion and
XX their size compared by agarose gel electrophoresis. Four clones had
XX insert sizes of approx. 400bp the others between 250-300bp. The inserts

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CC of the 4 largest clones were then sequenced and found to differ only in
CC the length of their 5' and 3' UTR's. The longest sequence was identified
CC as Rs-AFP1 (AAQ38650). Rs-AFP2 was seen to differ by only 2 amino acids
CC from Rs-AFP1, so the Rs-AFP1 cDNA was transformed to the Rs-AFP2
CC nucleotide sequence by PCR assisted site directed mutagenesis. (Updated
CC on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 261 BP; 67 A; 55 C; 59 G; 80 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,938-45 Length: 261
Score: 433.00 Matches: 78
Percent Similarity: 98.8% Conservative: 1
Best Local Similarity: 97.5% Mismatches: 1
Query Match: 98.0% Indels: 0
DB: 2 Gaps: 0

US-09-759-584-49 (1-80) x AAQ38652 (1-261)

QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20
Db 16 ATGGCTAAGTTGGTCCATCGACATCTTTTGGCTGCTGCTGCTGCTGCTGCT 75
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
Db 76 TTCGAAGCACCACCAATGTTGGGAAGCACAGAAAGTTGTGGAAAGGCGCAAGTGGGACATGG 135
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysAlaAsnLeuGluLysAla 60
Db 136 TCAGGAGTCTGTGGAAACAATTAACGCATGCAAGATCAGTGCAATTAACCTTGAGAAAGCA 195
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysAlaCysTyrPheProCys 80
Db 196 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAAAGTGTATCTGCTACTTTCCTTCT 255

RESULT 6
AAQ70130
ID AAQ70130 standard; cDNA; 288 BP.
XX
AC AAQ70130;
XX
DT 25-MAR-2003 (revised)
DT 14-FEB-1995 (first entry)
XX
DE Antimicrobial Rs-AFP2.
XX
KW Antimicrobial; Rs-AFP2; symbiosis; disease-resistance; fungus-resistance;
KW Clavibacter xyli subsp. cynodontis; Cxc; crop improvement; endophyte;
KW PCR; polymerase chain reaction; mutagenesis; ss.
XX
OS Raphanus sativus.
XX
XX WO9416076-A1.
XX
XX 21-JUL-1994.
XX
XX 05-JAN-1994; 94WO-GB0000012.
XX
XX 08-JAN-1993; 93GB-00000281.
XX
XX (ZENE ) ZENECA LTD.
XX
XX Dubook AC, Powell KA, Rees SB;
XX
XX WPI; 1994-249223/30.
XX
XX P-PSDB; AAR57327.
XX
XX Antimicrobial protein producing endo-symbiotic microorganisms - is
XX produced by combining nucleic acids encoding the protein with an
XX endophyte, useful for protecting plant hosts from eep. fungal disease.
XX
XX Disclosure; Page 33; 39pp; English.
XX
XX

```

CC Plant-derived antimicrobial proteins are expressed in endosymbiotic  
 CC Clavibacter xyli subsp. cynodotis (Cxc). Plants or seeds treated with  
 CC recombinant Cxc are protected against fungal disease. A suitable  
 CC antimicrobial protein is Rs-AFP1 from R. sativus. The full-length cDNA  
 CC sequence of PCR assisted site-directed mutagenesis of Rs-AFP2 is given in  
 CC AAQ70130 and the deduced amino acid sequence in AAR57327. (Updated on 25-  
 CC MAR-2003 to correct PN field.)

XX Sequence 288 BP; 70 A; 66 C; 69 G; 83 T; 0 U; 0 Other;

Alignment Scores: 3,35e-45 Length: 288  
 Pred. No.: 432.00 Matches: 78  
 Score: 98.8% Conservativity: 1  
 Percent Similarity: 97.5% Mismatches: 1  
 Best Local Similarity: 98.0% Indels: 0  
 Query Match: 2 Gaps: 0  
 DB:

US-09-759-584-49 (1-80) x AAQ70130 (1-288)

QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20  
 Db 43 ATGGCTAAGTTTGGTCCATCGCACTCTTTTGGTCTCTTCTTTTGGTCT 102  
 QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40  
 Db 103 TTCGAAGCACCACCAATGGTGAAGCACAGAACTTGTGCAAGGCCAAGTGGACATGG 162  
 QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60  
 Db 163 TCAGGAGTCTGTGGAACAATACGCATGCAAGATCAGTGCATTAGACTTGGAAGAAGCA 222  
 QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
 Db 223 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAGTGTATCTGCTACTTCTTGT 282

RESULT 7

ID ADC51221 standard; DNA; 394 BP.

AC ADC51221;

XX 18-DEC-2003 (first entry)

XX Brassica oleracea defensin protein coding sequence.

XX antimicrobial protein; defensin; transgenic plant;  
 KW composite disease resistance; pathogenic bacteria;  
 KW rice white leaf blight; brown-stripe disease; glume blight;  
 KW seedling damping-off disease; filamentous fungi; rice blight;  
 KW sheath blight disease; leaf blight; gene; ds.

XX Brassica oleracea.

XX Key Location/Qualifiers  
 FH 1..243  
 FT /\*tag= a  
 FT /product= "Brassica oleracea defensin protein"

XX JP2003088379-A.

XX 25-MAR-2003.

XX 18-SEP-2001; 2001JP-00283117.

XX 18-SEP-2001; 2001JP-00283117.

XX (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.

XX WPI; 2003-621123/59.

DR P-PSDB; ADC51222.

XX Novel protein from Brassica campestris, useful as antimicrobial against

PT plant pathogenic filamentous fungi or pathogenic bacteria, especially for  
 PT treating e.g. rice white leaf blight and sheath blight disease.

XX Claim 3; SEQ ID NO 1; 34pp; Japanese.

XX The invention comprises the amino acid and coding sequences of  
 CC antimicrobial (defensin) proteins from Brassica. The DNA and protein  
 CC sequences of the invention are useful for producing transgenic plants  
 CC with composite disease resistance, especially resistant to diseases  
 CC caused by pathogenic bacteria, such as: rice white leaf blight, brown-  
 CC stripe disease, glume blight, and seedling damping-off disease. As well  
 CC as diseases caused by filamentous fungi, such as: rice blight, sheath  
 CC blight disease, and leaf blight. The present DNA sequence encodes a  
 CC Brassica defensin protein of the invention.

XX Sequence 394 BP; 116 A; 71 C; 82 G; 125 T; 0 U; 0 Other;

Alignment Scores: 6.86e-45 Length: 394  
 Pred. No.: 432.00 Matches: 78  
 Score: 97.5% Conservativity: 0  
 Percent Similarity: 97.5% Mismatches: 2  
 Best Local Similarity: 97.7% Indels: 0  
 Query Match: 10 Gaps: 0  
 DB:

US-09-759-584-49 (1-80) x ADC51221 (1-394)

QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20  
 Db 1 ATGGCTAAGTTTGGTCCATCGCACTCTTTTGGTCTCTTCTTTTGGTCT 60  
 QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40  
 Db 61 CTCGAAGCACCACCAATGGTGAAGCACAGAACTTGTGCGAGAGGCCAAGTGGACATGG 120  
 QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60  
 Db 121 TCAGGAGTCTGTGGAACAATACGCATGCAAGATCAGTGCATTAAACCTTGAGAAGCA 180  
 QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
 Db 181 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAGTGTATTTGCTACTTCTTGT 240

RESULT 8

ADU71300

ID ADU71300 standard; cDNA; 394 BP.

XX AC ADU71300;

XX 10-FEB-2005 (first entry)

XX Brassica oleracea defensin protein coding sequence - SEQ ID 1.

XX antimicrobial; plant disease resistance; gene; ss; defensin.

XX Brassica oleracea.

XX Key Location/Qualifiers  
 FH 1..243  
 FT /\*tag= a  
 FT /product= "Brassica oleracea defensin protein - SEQ ID 2"

XX JP2004329215-A.

XX 25-NOV-2004.

XX 07-JUN-2004; 2004JP-00168986.

XX 18-SEP-2001; 2001JP-00283117.

XX (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.

XX WPI; 2004-809169/80.

DR P-PSDB; ADU71301.  
 XX Novel Brassica sp. derived protein having antimicrobial activity, useful  
 PT for producing multiple disease resistant plants.  
 XX Example 2; SEQ ID NO 1; 16pp; Japanese.  
 PS  
 XX The invention comprises the amino acid and coding sequence of an  
 CC antimicrobial protein obtained from Brassica sp. The DNA and protein  
 CC sequences of the invention are useful in the production of a multiple  
 CC disease resistant plant. The present cDNA sequence encodes the Brassica  
 CC oleracea defensin protein.  
 XX  
 SQ Sequence 394 BP; 116 A; 71 C; 82 G; 125 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 6.86e-45 Length: 394  
 Score: 432.00 Matches: 78  
 Percent Similarity: 97.5% Conservative: 0  
 Best Local Similarity: 97.5% Mismatches: 2  
 Query Match: 97.7% Indels: 0  
 DB: 13 Gaps: 0

US-09-759-584-49 (1-80) x ADU71300 (1-394)  
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 Db 1 ATGGCTAAGTTTGTGTCCTCATGTCCTCTTTTGTCTCTTTTGTCTCTTTTGTCTCT 60  
 QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40  
 Db 61 CTCGAGCACCACCAACATGGTGGAGGCACAGAGCTTGTGGAGAGGCCAAGTGGGACATGG 120  
 QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60  
 Db 121 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 180  
 QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
 Db 181 CGACATGGATCTTGCAACTATGTCTTCCAGCTCACAAGTGTATTTGCTACTTCCCTTGT 240

RESULT 9  
 ADC51223  
 ID ADC51223 standard; DNA; 426 BP.  
 AC ADC51223;  
 XX 18-DEC-2003 (first entry)  
 DE Brassica defensin protein coding sequence.  
 XX antimicrobial protein; defensin; transgenic plant;  
 KW composite disease resistance; pathogenic bacteria;  
 KW rice white leaf blight; brown-stripe disease; glume blight;  
 KW seedling damping-off disease; filamentous fungi; rice blight;  
 KW sheath blight disease; leaf blight; gene; ds.  
 XX Brassica sp.  
 OS  
 XX Key Location/Qualifiers  
 FT CDS 1..243  
 FT /\*tag= a  
 FT /product= "Brassica defensin protein"  
 XX  
 PN JP2003088379-A.  
 XX 25-MAR-2003.  
 XX 18-SEP-2001; 2001JP-00283117.  
 XX 18-SEP-2001; 2001JP-00283117.  
 XX (DOKU-) DOKURITSU GYOSSEI HOJIN NOGYO SEIBUTSU SH.

XX WPI; 2003-621123/59.  
 DR P-PSDB; ADC51224.  
 XX Novel protein from Brassica campestris, useful as antimicrobial against  
 PT plant pathogenic filamentous fungi or pathogenic bacteria, especially for  
 PT treating e.g. rice white leaf blight and sheath blight disease.  
 XX Claim 3; SEQ ID NO 3; 34pp; Japanese.  
 XX The invention comprises the amino acid and coding sequences of  
 CC antimicrobial (defensin) proteins from Brassica. The DNA and protein  
 CC sequences of the invention are useful for producing transformed plants  
 CC with composite disease resistance, especially resistant to diseases  
 CC caused by pathogenic bacteria, such as: rice white leaf blight, brown-  
 CC stripe disease, glume blight, and seedling damping-off disease. As well  
 CC as diseases caused by filamentous fungi, such as: rice blight, sheath  
 CC blight disease, and leaf blight. The present DNA sequence encodes a  
 CC Brassica defensin protein of the invention.  
 XX  
 SQ Sequence 426 BP; 142 A; 72 C; 84 G; 128 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 5.8e-44 Length: 426  
 Score: 425.00 Matches: 77  
 Percent Similarity: 96.2% Conservative: 0  
 Best Local Similarity: 96.2% Mismatches: 3  
 Query Match: 96.2% Indels: 0  
 DB: 10 Gaps: 0

US-09-759-584-49 (1-80) x ADC51223 (1-426)  
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 Db 1 ATGGCCAGTTTGTGTCATCATTTGCCACACCTTTTGTCTCTTGTCTCTTTTAGCTGCT 60  
 QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40  
 Db 61 TTCGAGGCCACCAACATGGTGGAGGCACACAGAGTTTGTGGAGAGGCCAAGTGGGACATGG 120  
 QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60  
 Db 121 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCTTGAGAAAGCA 180  
 QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
 Db 181 CGACATGGATCTTGCAACTATGTCTTCCAGCTCACAAGTGTATTTGCTACTTCCCTTGT 240

RESULT 10  
 ADU71302  
 ID ADU71302 standard; DNA; 426 BP.  
 XX AC ADU71302;  
 XX 10-FEB-2005 (first entry)  
 DE Brassica antimicrobial protein coding sequence - SEQ ID 3.  
 XX antimicrobial; plant disease resistance; gene; ds.  
 OS Brassica sp.  
 XX Key Location/Qualifiers  
 FT CDS 1..243  
 FT /\*tag= a  
 FT /product= "Brassica antimicrobial protein - SEQ ID 4"  
 XX  
 PN JP2004329215-A.  
 XX 25-NOV-2004.  
 XX 07-JUN-2004; 2004JP-00168986.  
 XX

```

PR 18-SEP-2001; 2001JP-00283117.
XX
XX (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
XX
XX WPI; 2004-809169/80.
XX P-PSDB; ADU71303.
XX
XX Novel Brassica sp. derived protein having antimicrobial activity, useful
XX for producing multiple disease resistant plants.
XX
XX Claim 3; SEQ ID NO 3; 16pp; Japanese.
XX
XX The invention comprises the amino acid and coding sequence of an
XX antimicrobial protein obtained from Brassica sp. The DNA and protein
XX sequences of the invention are useful in the production of a multiple
XX disease resistant plant. The present DNA sequence encodes the Brassica
XX antimicrobial protein of the invention.
XX
XX SQ Sequence 426 BP; 142 A; 72 C; 84 G; 128 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 5.8e-44 Length: 426
XX Score: 425.00 Matches: 77
XX Percent Similarity: 96.2% Conservative: 0
XX Best Local Similarity: 96.2% Mismatches: 3
XX Query Match: 96.2% Indels: 0
XX DB: 13 Gaps: 0
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XX US-09-759-584-49 (1-80) x ADU71302 (1-426)
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XX QY 1 MetAlaLysPheAlaSerIleIleAlaLeuPheAlaAlaLeuValLeuPheAlaAla 20
XX Db 1 ATGGCCAAAGTTTGTTGTTATCATTCGCCACCTTTTTCCTGCTTCTTTAGCTGCT 60
XX
XX QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTTP 40
XX Db 61 TTCGAGGCACCACCAATGTTGGAGCACAGAAAGTTGTCGAGAGGCCAAGTGGACATGG 120
XX
XX QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
XX Db 121 TCAGGAGTCTGTGGAACAATAACGCATCGCAGATCAGTGCATTAACCTTGAGAAAGCA 180
XX
XX QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
XX Db 181 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAGTGTATTGCTACTTCCCTTGT 240
XX
XX RESULT 11
XX AAA53190
XX ID AAA53190 standard; DNA; 449 BP.
XX AC
XX AA53190;
XX
XX DT 06-OCT-2000 (first entry)
XX
XX DE Raphanus sativus antibacterial protein radishin encoding DNA SEQ ID NO:1.
XX
XX KW Raphanus sativus; antibacterial; plant; resistance; paddy; radishin;
XX pathogenic microbe; radish; rice blast disease; ds.
XX
XX OS Raphanus sativus.
XX
XX PN JP2000116379-A.
XX
XX PD 25-APR-2000.
XX
XX PF 09-OCT-1998; 98JP-00288472.
XX
XX PR 09-OCT-1998; 98JP-00288472.
XX (TOYA-) TOYAMA KEN.
XX
XX WPI; 2000-389821/34.
XX P-PSDB; AAY91117.
XX

XX Isolated DNA from Raphanus sativus used to transform a microbe and a
XX plant to produce an antibacterial protein used to increase resistance of
XX rice paddy against pathogenic microbes.
XX
XX Claim 1; Page 4; 7pp; Japanese.
XX
XX The present sequence encodes an antibacterial protein, designated
XX radishin, isolated from Raphanus sativus (radish). A phage or plasmid
XX comprising radishin can be used for increasing resistance of paddy and
XX rice blast disease against pathogenic microbes
XX
XX SQ Sequence 449 BP; 126 A; 78 C; 94 G; 151 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 1.11e-43 Length: 449
XX Score: 423.00 Matches: 75
XX Percent Similarity: 97.5% Conservative: 3
XX Best Local Similarity: 93.8% Mismatches: 2
XX Query Match: 95.7% Indels: 0
XX DB: 3 Gaps: 0
XX
XX US-09-759-584-49 (1-80) x AAA53190 (1-449)
XX
XX QY 1 MetAlaLysPheAlaSerIleIleAlaLeuPheAlaAlaLeuValLeuPheAlaAla 20
XX Db 41 ATGGCTAAAGTTTGCTTCCATCATTCCTTCTTCGCTGCTCTTGTCTGTTTTTCTGCT 100
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XX QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTTP 40
XX Db 101 TTCGAAGCACCAACCAATGTTGGAGCACAGAAAGTTGTCAGAGGCCAAGTGGACATGG 160
XX
XX QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
XX Db 161 TCAGGAGTCTGTGGAATAATAACGCATCGCAGATCAGTGCATTCGACTTGAGAAAGCA 220
XX
XX QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
XX Db 221 CGACATGGTCTTGCACACTATGCTTCCAGCTCACAGTGTATCTGTTATTTCCCTTGT 280
XX
XX RESULT 12
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XX ID AAZ99339 standard; DNA; 575 BP.
XX AC
XX AAZ99339;
XX
XX DT 03-JUL-2000 (first entry)
XX
XX DE DNA encoding a fusion protein of DmAMP1 and RsAPP2.
XX
XX KW Antimicrobial protein; AMP1; transgenic plant; linker propeptide;
XX protein expression; plant defensin; RsAPP2; antifungal protein; AFP2; ss.
XX
XX OS Synthetic.
XX
XX OS Dahlia merckii.
XX Unidentified.
XX
XX FH Key Location/Qualifiers
XX CDS 3...566
XX FT /*tag= a
XX FT /product= "fusion protein of DmAMP1 and RsAPP2"
XX
XX PN WO200011175-A1.
XX
XX PD 02-MAR-2000.
XX
XX PF 17-AUG-1999; 99WO-GB002716.
XX
XX PR 18-AUG-1998; 98GB-00018001.
XX 04-DEC-1998; 98GB-00026753.
XX (ZENE) ZENECA LTD.
XX
XX
```



PN JP11313678-A.  
XX 16-NOV-1999.  
XX 30-APR-1998; 98JP-00121303.  
XX 30-APR-1998; 98JP-00121303.  
XX (IWAT-) IWATE KEN.  
XX WPI; 2000-057353/05.  
XX P-PSDB; AAY57564.  
XX An antibacterial protein gene of Wasabia japonica - useful as a food- or feed-additive.  
XX Claim 3; Page 12-13; 16pp; Japanese.  
XX The present sequence encodes an antibacterial protein isolated from Wasabia japonica. The antibacterial protein can be used as a food or feed additive. (Updated on 15-SEP-2003 to standardise OS field)  
XX Sequence 414 BP; 108 A; 79 C; 80 G; 147 T; 0 U; 0 Other;  
SQ  
Alignment Scores:  
Pred. No.: 1.03e-41 Length: 414  
Score: 407.00 Matches: 72  
Percent Similarity: 96.2% Conservative: 5  
Best Local Similarity: 90.0% Mismatches: 3  
Query Match: 92.1% Indels: 0  
DB: 3 Gaps: 0  
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Db 1 ATGGCTAAGTTTGGCTTCTATCATCGCTCTCTTCGCTGCTTCTTCTTCTGCT 60  
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40  
Db 61 TTGAGACCACTCAATGGTGGAGCGCAGAGTTGTGCGAGAGTCAAGTGGGACATGG 120  
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60  
Db 121 TCAGGAGTCTGTGGAAACAACAATGCGTGCAGAAATCAGTGCATCAACCTTGAGGGAGCA 180  
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
Db 181 CGACATGGATCTTGCACATATATCTTCCCATATATCAGAGATGATCTGTACTTCCCATGT 240  
RESULT 15  
ABZ14241  
ID ABZ14241 standard; DNA; 243 BP.  
XX  
AC ABZ14241;  
XX  
DT 21-JAN-2003 (first entry)  
XX  
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2046.  
XX  
KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.  
XX  
OS Arabidopsis thaliana.  
XX  
PN WO200216555-A2.  
XX  
PD 28-FEB-2002.  
XX  
PF 24-AUG-2001; 2001WO-US026685.  
XX  
PR 24-AUG-2000; 2000US-0227866P.  
XX  
PR 26-JAN-2001; 2001US-0264647P.  
XX  
PR 22-JUN-2001; 2001US-0300111P.

XX (SCRI ) SCRIPPS RES INST.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX  
PI Harper JF, Kreps J, Wang X, Zhu T;  
XX  
DR WPI; 2002-304127/34.  
XX  
PT Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.  
XX  
PS Claim 144; SEQ ID NO 2046; 577pp + Sequence Listing; English.  
XX  
CC The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) CC detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the CC production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is CC not represented in the printed specification but is based on sequence CC information supplied to Derwent by the European Patent Office  
XX  
SQ Sequence 243 BP; 62 A; 57 C; 58 G; 66 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 1.59e-41 Length: 243  
Score: 403.00 Matches: 71  
Percent Similarity: 95.0% Conservative: 5  
Best Local Similarity: 88.8% Mismatches: 4  
Query Match: 91.2% Indels: 0  
DB: 6 Gaps: 0  
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Db 1 ATGGCTAAGTTTGGCTTCTTCCATCATCACCTTATCTTCGCTGCTTCTTCTTCTGCT 60  
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40  
Db 61 TTTCGACGACCGGCAATGGTGGAGCACAGAGTTGTGCGAGAGCCAGTGGGACATGG 120  
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60  
Db 121 TCAGGGGTTTGGGAAACAGTAATGATGATGATGATGATGATGATGATGATGATGATGAT 180  
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
Db 181 AAACATGGATCATGCACTATGCTTCCAGCACACAGTGTATCTGTACGTCCCATGT 240  
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Job time : 453 secs

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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

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Run on: May 10, 2006, 06:02:00 ; Search time 3003.5 Seconds  
(without alignments)  
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Title: US-09-759-584-49

Perfect score: 442

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
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Searched: 41078325 seqs, 23393541228 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%

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#### SUMMARIES

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4	436	98.6	421	6	CD826491 CN826491 EN25.064A
5	436	98.6	421	6	CD831111 CN831111 EN40.058A
6	436	98.6	421	6	CD833977 CN833977 EN45.040D
7	436	98.6	422	6	CD833983 CN833983 EN45.040D

8	436	98.6	426	6	CD827413	CD827413	BN25.067G
9	436	98.6	438	6	CD831294	CD831294	BN40.058N
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13	436	98.6	456	7	CN726661	CN726661	3ETMS UP
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40	427	96.6	421	6	CD837517	CD837517	BN45.052I
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#### ALIGNMENTS

RESULT 1  
CN826227  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

CN826227  
EL1386 Brassica embryo library (EL)  
EL1386 complete, mRNA sequence.  
CN826227.1 GI:65296011  
EST.  
Brassica napus (rape)  
Brassica napus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

Sharpe,A.G., Gjetvaj,B., Durkin,J. and Lydiate,D.J.  
1 (bases 1 to 413)  
Unpublished (2004)  
Contact: Sharpe, A.G.  
Molecular Genetics  
Agriculture & Agri-Food Canada  
107 Science Place, Saskatoon, Saskatchewan, Canada, S7N0X2  
Tel: 306 956 7271  
Fax: 306 956 7247  
Email: sharpe@agr.gc.ca  
Seq primer: M13 Forward and T7.  
Location/Qualifiers  
1. 413  
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/culturivar="DH12075 (double haploid line from Cresor x Westar cross)"

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/clone_lib="Brassica embryo library (EL)"
/note="Organ: Embryos without seed coat; Vector: pSPORT1
(modified: GCGCGGCCCGACTAGTGAGTC*cgagcgtgggtgcac);
Site_1: NotI; Site_2: SalI; Seeds were collected by Dr.
Francois Ouellet when they were still very green (mid to
large stage, cotyledons were formed). The seed coats were
removed and the remaining tissue was used for cDNA library
construction. mRNA was poly-A primed using SuperScript
plasmid system cDNA Synthesis and Cloning kit (Invitrogen)
After initial screening, the most abundant redundant
clones were screened out using 22 oligos designed to match
napins (including albumins), cruciferins, oleosins,
trypsin inhibitor 2, cytosolic GAPDH, cyclophilins, HSP70,
desaturase, and CAB (LHCP)."
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## ORIGIN

Alignment Scores:  
Pred. No.: 1.65e-41 Length: 413  
Score: 436.00 Matches: 79  
Percent Similarity: 98.8% Conservative: 0  
Best Local Similarity: 98.8% Mismatches: 1  
Query Match: 98.6% Indels: 0  
DB: 7 Gaps: 0

US-09-759-584-49 (1-80) x CN826227 (1-413)

QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaLeuValLeuPheAlaLa 20  
DB 28 ATGGCTAAGTTGCTTCCATCATTCCTTCTGCTCTTTGCTCTTTGCTCTGT 87  
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40  
DB 88 CTCGAAGCACCACCAATGTTGGAGCACAGAGTTGTGCGAGAGCCCAAGTGGACATGG 147  
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60  
DB 148 TCAGGAGTCTGTGGAAACAATACGCATGCAAGATCAGTGCATTAACCTTGAGAAAGCA 207  
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
DB 208 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAGTGATTGCTTCTCTTGT 267

## RESULT 2

CD832625 418 bp mRNA linear EST 10-JUL-2003  
LOCUS BN40.064A14F011227 BN40 Brassica napus cDNA clone BN40064A14, mRNA  
DEFINITION sequence.

ACCESSION CD832625

VERSION CD832625.1 GI:32514565

KEYWORDS EST.

SOURCE Brassica napus (rape)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 418)

Genoplatte.

Genoplatte, a major partnership french program in plant genomics

Unpublished (2003)

Contact: Genoplatte

Genoplatte

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>  
and <http://genoplatte-info.infobiogen.fr>).

## FEATURES

Location/Qualifiers

1. .418

source

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/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet Neuf"
/db_xref="taxon:3708"
/clone="BN40064A14"
/tissue_type="seed"
/clone_lib="BN40"
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## ORIGIN

Alignment Scores:  
Pred. No.: 1.67e-41 Length: 418  
Score: 436.00 Matches: 79  
Percent Similarity: 98.8% Conservative: 0  
Best Local Similarity: 98.8% Mismatches: 1  
Query Match: 98.6% Indels: 0  
DB: 6 Gaps: 0

US-09-759-584-49 (1-80) x CD832625 (1-418)

QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaLaLeuValLeuPheAlaLa 20  
DB 53 ATGGCAAGTTGCTTCCATCATTCCTTCTGCTCTTTGCTCTTTGCTCTGT 112  
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40  
DB 113 CTCGAAGCACCACCAATGTTGGAGCACAGAGTTGTGCGAGAGCCCAAGTGGACATGG 172  
QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60  
DB 173 TCAGGAGTCTGTGGAAACAATACGCATGCAAGATCAGTGCATTAACCTTGAGAAAGCA 232  
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
DB 233 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAGTGATTGCTTCTCTTGT 292

## RESULT 3

CD833944

LOCUS

DEFINITION

sequence.

ACCESSION CD833944

VERSION CD833944.1 GI:32515884

KEYWORDS EST.

SOURCE Brassica napus (rape)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 420)

Genoplatte.

Genoplatte, a major partnership french program in plant genomics

Unpublished (2003)

Contact: Genoplatte

Genoplatte

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>  
and <http://genoplatte-info.infobiogen.fr>).

## FEATURES

source

1. .420

/organism="Brassica napus"

/mol\_type="mRNA"

/cultivar="Jet Neuf"

/db\_xref="taxon:3708"

/clone="BN40064A14"

/tissue\_type="seed"

/clone\_lib="BN45"

## ORIGIN

Alignment Scores:  
Pred. No.: 1.68e-41 Length: 420

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Score:          436.00      Matches:          79
Percent Similarity: 98.8%      Conservative: 0
Best Local Similarity: 98.8%      Mismatches: 1
Query Match:      98.6%      Indels: 0
DB:               6      Gaps: 0

US-09-759-584-49 (1-80) x CD833944 (1-420)

QY      1 MetAlaLysPheAlaSerIleLeAlaLeuPheAlaLeuValLeuPheAlaLa 20
Db      50 ATGGCTAAGTTGCTTCCATCATTCGCCCTACTTTTGGCTGCTCTTGTGCTGCT 109

QY      21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
Db      110 CTCGAGACCAACAACAAATGTTGGAGCACAGAAAGTTGTGCGAGAGGCCAAGTGGACATGG 169

QY      41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
Db      170 TCAGGAGTCTGTGGAACAACAATTAACGATCGAAGATCAAGTGCATTAACCTTGAGAAAGCA 229

QY      61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
Db      230 CGACATGGATCTTGGCAACTATGCTTCCAGCTCACAAGTGATTTGCTACTTCCCTTGT 289

RESULT 4
CD826491      421 bp mRNA linear EST 10-JUL-2003
LOCUS      BN25_064A05F020416 BN25 Brassica napus cDNA clone BN25064A05, mRNA
DEFINITION      sequence.
ACCESSION      CD826491
VERSION      CD826491.1 GI:32508431
KEYWORDS      EST.
SOURCE      Brassica napus (rape)
ORGANISM      Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE      1 (bases 1 to 421)
AUTHORS      Genoplante.
TITLE      Genoplante, a major partnership french program in plant genomics
JOURNAL      Unpublished (2003)
COMMENT      Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).

FEATURES
source
1..421
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet Neuf"
/db_xref="taxon:3708"
/clone="BN25064A05"
/tissue_type="seed"
/clone_lib="BN25"

ORIGIN
Alignment Scores:
Pred. No.:      1.69e-41      Length:      421
Score:          436.00      Matches:      79
Percent Similarity: 98.8%      Conservative: 0
Best Local Similarity: 98.8%      Mismatches: 1
Query Match:      98.6%      Indels: 0
DB:             6      Gaps: 0

US-09-759-584-49 (1-80) x CD826491 (1-421)

QY      1 MetAlaLysPheAlaSerIleLeAlaLeuPheAlaLeuValLeuPheAlaLa 20
Db      51 ATGGCTAAGTTGCTTCCATCATTCGCCCTACTTTTGGCTGCTCTTGTGCTGCT 110

QY      21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
Db      111 CTCGAGACCAACAACAAATGTTGGAGCACAGAAAGTTGTGCGAGAGGCCAAGTGGACATGG 170

QY      41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
Db      171 TCAGGAGTCTGTGGAACAACAATTAACGATCGAAGATCAAGTGCATTAACCTTGAGAAAGCA 230

QY      61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
Db      231 CGACATGGATCTTGGCAACTATGCTTCCAGCTCACAAGTGATTTGCTACTTCCCTTGT 290

RESULT 5
CD831111      421 bp mRNA linear EST 10-JUL-2003
LOCUS      BN40_058A09F011019 BN40 Brassica napus cDNA clone BN40058A09, mRNA
DEFINITION      sequence.
ACCESSION      CD831111
VERSION      CD831111.1 GI:32513051
KEYWORDS      EST.
SOURCE      Brassica napus (rape)
ORGANISM      Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE      1 (bases 1 to 421)
AUTHORS      Genoplante.
TITLE      Genoplante, a major partnership french program in plant genomics
JOURNAL      Unpublished (2003)
COMMENT      Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).

FEATURES
source
1..421
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet Neuf"
/db_xref="taxon:3708"
/clone="BN40058A09"
/tissue_type="seed"
/clone_lib="BN40"

ORIGIN
Alignment Scores:
Pred. No.:      1.69e-41      Length:      421
Score:          436.00      Matches:      79
Percent Similarity: 98.8%      Conservative: 0
Best Local Similarity: 98.8%      Mismatches: 1
Query Match:      98.6%      Indels: 0
DB:             6      Gaps: 0

US-09-759-584-49 (1-80) x CD831111 (1-421)

QY      1 MetAlaLysPheAlaSerIleLeAlaLeuPheAlaLeuValLeuPheAlaLa 20
Db      51 ATGGCTAAGTTGCTTCCATCATTCGCCCTACTTTTGGCTGCTCTTGTGCTGCT 110

QY      21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
Db      111 CTCGAGACCAACAACAAATGTTGGAGCACAGAAAGTTGTGCGAGAGGCCAAGTGGACATGG 170

QY      41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
Db      171 TCAGGAGTCTGTGGAACAACAATTAACGATCGAAGATCAAGTGCATTAACCTTGAGAAAGCA 230

QY      61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
Db      231 CGACATGGATCTTGGCAACTATGCTTCCAGCTCACAAGTGATTTGCTACTTCCCTTGT 290

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Db 231 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAAGTGATTTGCTACTTCCCTTGT 290

RESULT 6
CD833977
LOCUS
DEFINITION
CD833977 421 bp mRNA linear EST 10-JUL-2003
BN45.040D05F011019 BN45 Brassica napus cDNA clone BN45040D05, mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
EST.
CD833977.1 GI:32515917
Brassica napus (rape)
ORGANISM
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 421)
Genoplante, a major partnership french program in plant genomics
Genoplante.
Genoplante.
Unpublished (2003)
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
FEATURES
source
Location/Qualifiers
1..421
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet Neuf"
/db_xref="taxon:3708"
/clone="BN45040D05"
/tissue_type="seed"
/clone_lib="BN45"

ORIGIN
Alignment Scores:
Pred. No.: 1.69e-41 Length: 421
Score: 436.00 Matches: 79
Percent Similarity: 98.8% Conservative: 0
Best Local Similarity: 98.8% Mismatches: 1
Query Match: 98.6% Indels: 0
DB: 6 Gaps: 0

US-09-759-584-49 (1-80) x CD833977 (1-421)

QY 1 MetAlaLysPheAlaSerIleAlaLeuPheAlaAlaLeuValLeuPheAlaAla 20
|||||
Db 51 ATGGCTAAGTTTGCTTCCATCATGTCCTACTTTTGTGCTGCTTTTTCGCTGCT 110
|||||

QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
|||||
Db 111 CTCGAAGCACCACAATGTTGGAAGCACAGAAGTTGTGCGAGAGCGCAAGTGGGACATGG 170
|||||

QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
|||||
Db 171 TCAGGAGTCTGTGGAACAATAACGCATGCAAGAATCAGTGCATTAAACCTTGAGAAAGCA 230
|||||

QY 61 AtgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
|||||
Db 231 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAAGTGATTTGCTACTTCCCTTGT 290

RESULT 7
CD833983
LOCUS
DEFINITION
CD833983 422 bp mRNA linear EST 10-JUL-2003
BN45.040D11F011019 BN45 Brassica napus cDNA clone BN45040D11, mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
EST.
CD833983.1 GI:32515923
Brassica napus (rape)
ORGANISM
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 422)
Genoplante, a major partnership french program in plant genomics
Genoplante.
Genoplante.
Unpublished (2003)
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
FEATURES
source
Location/Qualifiers
1..422
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet Neuf"
/db_xref="taxon:3708"
/clone="BN45040D11"
/tissue_type="seed"
/clone_lib="BN45"

ORIGIN
Alignment Scores:
Pred. No.: 1.69e-41 Length: 422
Score: 436.00 Matches: 79
Percent Similarity: 98.8% Conservative: 0
Best Local Similarity: 98.8% Mismatches: 1
Query Match: 98.6% Indels: 0
DB: 6 Gaps: 0

US-09-759-584-49 (1-80) x CD833983 (1-422)

QY 1 MetAlaLysPheAlaSerIleAlaLeuPheAlaAlaLeuValLeuPheAlaAla 20
|||||
Db 51 ATGGCTAAGTTTGCTTCCATCATGTCCTACTTTTGTGCTGCTTTTTCGCTGCT 110
|||||

QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
|||||
Db 111 CTCGAAGCACCACAATGTTGGAAGCACAGAAGTTGTGCGAGAGCGCAAGTGGGACATGG 170
|||||

QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
|||||
Db 171 TCAGGAGTCTGTGGAACAATAACGCATGCAAGAATCAGTGCATTAAACCTTGAGAAAGCA 230
|||||

QY 61 AtgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
|||||
Db 231 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAAGTGATTTGCTACTTCCCTTGT 290

RESULT 8
CD827413
LOCUS
DEFINITION
CD827413 426 bp mRNA linear EST 10-JUL-2003
BN25.067G02F020123 BN25 Brassica napus cDNA clone BN25067G02, mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
EST.
CD827413.1 GI:32509353
Brassica napus (rape)
ORGANISM
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 426)
Genoplante, a major partnership french program in plant genomics
Genoplante.
Unpublished (2003)
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
```

Tel: 33 1 69 47 54 00  
 Fax: 33 1 69 47 54 10  
 This sequence has been generated in the framework of the french  
 plant genomics programme 'Genoplante' (<http://www.genoplante.com>)  
 and <http://genoplante-info.infobiogen.fr>.

## FEATURES

source  
 Location/Qualifiers  
 1. .426  
 /organism="Brassica napus"  
 /mol\_type="mRNA"  
 /cultivar="Jet Neuf"  
 /db\_xref="taxon:3708"  
 /clone="BN25067G02"  
 /tissue\_type="seed"  
 /clone\_lib="BN25"

## ORIGIN

Alignment Scores:  
 Pred. No.: 1.71e-41 Length: 426  
 Score: 436.00 Matches: 79  
 Percent Similarity: 98.8% Conservative: 0  
 Best Local Similarity: 98.8% Mismatches: 1  
 Query Match: 98.6% Indels: 0  
 DB: 6 Gaps: 0

US-09-759-584-49 (1-80) x CD827413 (1-426)

QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20  
 |||||  
 Db 51 ATGGCTAAGTTGCTTCCATCATTTGCCCTACTTTTGGCTCTTGTCTTTTGGCTGCT 110  
 |||||

QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40  
 |||||  
 Db 111 CTCGAAGCACCACCAATGCTGGAAGCACAGAAGTTGTGCGAGAGCCAAAGTGGGACATGG 170  
 |||||

QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60  
 |||||  
 Db 171 TCAGGAGTCTGTGGAACCAATACGCATGCAAGATCAGTGCATTAACCTTCGAGAAGCA 230  
 |||||

QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
 |||||  
 Db 231 CGACATGGATCTTGCACTATGTCTCCAGCTCACAAGTGATTTGCTACTTCCCTTGT 290  
 |||||

RESULT 9  
 CD831294  
 LOCUS  
 DEFINITION  
 BN40.058N13F011019 BN40 Brassica napus cDNA clone BN40058N13, mRNA  
 sequence.  
 ACCESSION  
 CD831294  
 VERSION  
 CD831294.1 GI:32513234  
 KEYWORDS  
 EST.  
 SOURCE  
 Brassica napus (rape)  
 ORGANISM  
 Brassica napus  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE  
 1 (bases 1 to 438)  
 Genoplante.  
 Genoplante, a major partnership french program in plant genomics  
 Unpublished (2003)  
 CONTACT  
 Genoplante  
 93, rue Henri Rochefort 91025 EVRY CEDEX France  
 Tel: 33 1 69 47 54 00  
 Fax: 33 1 69 47 54 10  
 This sequence has been generated in the framework of the french  
 plant genomics programme 'Genoplante' (<http://www.genoplante.com>)  
 and <http://genoplante-info.infobiogen.fr>.

## FEATURES

source  
 Location/Qualifiers  
 1. .438  
 /organism="Brassica napus"  
 /mol\_type="mRNA"  
 /cultivar="Jet Neuf"  
 /db\_xref="taxon:3708"

/clone="BN40058N13"  
 /tissue\_type="seed"  
 /clone\_lib="BN40"

## ORIGIN

Alignment Scores:  
 Pred. No.: 1.78e-41 Length: 438  
 Score: 436.00 Matches: 79  
 Percent Similarity: 98.8% Conservative: 0  
 Best Local Similarity: 98.8% Mismatches: 1  
 Query Match: 98.6% Indels: 0  
 DB: 6 Gaps: 0

US-09-759-584-49 (1-80) x CD831294 (1-438)

QY 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20  
 |||||  
 Db 51 ATGGCTAAGTTGCTTCCATCATTTGCCCTACTTTTGGCTCTTGTCTTTTGGCTGCT 110  
 |||||

QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40  
 |||||  
 Db 111 CTCGAAGCACCACCAATGCTGGAAGCACAGAAGTTGTGCGAAGGCCAAAGTGGGACATGG 170  
 |||||

QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60  
 |||||  
 Db 171 TCAGGAGTCTGTGGAACCAATACGCATGCAAGATCAGTGCATTAACCTTCGAGAAGCA 230  
 |||||

QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80  
 |||||  
 Db 231 CGACATGGATCTTGCACTATGTCTCCAGCTCACAAGTGATTTGCTACTTCCCTTGT 290  
 |||||

RESULT 10  
 CD831479  
 LOCUS  
 DEFINITION  
 BN40.059J13F011208 BN40 Brassica napus cDNA clone BN40059J13, mRNA  
 sequence.  
 ACCESSION  
 CD831479  
 VERSION  
 CD831479.1 GI:32513419  
 KEYWORDS  
 EST.  
 SOURCE  
 Brassica napus (rape)  
 ORGANISM  
 Brassica napus  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE  
 1 (bases 1 to 438)  
 Genoplante.  
 Genoplante, a major partnership french program in plant genomics  
 Unpublished (2003)  
 CONTACT  
 Genoplante  
 93, rue Henri Rochefort 91025 EVRY CEDEX France  
 Tel: 33 1 69 47 54 00  
 Fax: 33 1 69 47 54 10  
 This sequence has been generated in the framework of the french  
 plant genomics programme 'Genoplante' (<http://www.genoplante.com>)  
 and <http://genoplante-info.infobiogen.fr>.

## FEATURES

source  
 Location/Qualifiers  
 1. .438  
 /organism="Brassica napus"  
 /mol\_type="mRNA"  
 /cultivar="Jet Neuf"  
 /db\_xref="taxon:3708"  
 /clone="BN40059J13"  
 /tissue\_type="seed"  
 /clone\_lib="BN40"

## ORIGIN

Alignment Scores:  
 Pred. No.: 1.78e-41 Length: 438  
 Score: 436.00 Matches: 79  
 Percent Similarity: 98.8% Conservative: 0  
 Best Local Similarity: 98.8% Mismatches: 1  
 Query Match: 98.6% Indels: 0

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DB:                                     6          Gaps:          0
US-09-759-584-49 (1-80) x CD831479 (1-438)

QY  1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  51 ATGGCTAAGTTTGCTTCCATCATTCGCCCTACTTTTGGCTGCTCTTGTCTCTTTCGCTGCT 110

QY  21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTTP 40
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  111 CTCGAAGCACCACCAATGTTGGAAGCACAGAAGTTGTGCGAGAGGCCAAGTGGGACATGG 170

QY  41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  171 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGATCAGTCATTAACCTTGAGAAGCA 230

QY  61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  231 CGACATGGATCTTGCAACTATGTCTTCCAGCTCACAAAGTGTATTGTCTACTTCCCTTGT 290

RESULT 11
CD834008
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CD834008
BN45.040E18F011019 BN45 Brassica napus cDNA clone BN45040E18, mRNA
sequence.
CD834008
CD834008.1 GI:32515948
EST.
Brassica napus (rape)
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 453)

REFERENCE
Tsang,E.
Gene expression in seed germination in Brassica napus
Unpublished (2004)
Contact: Ed Tsang
Plant Natural Products
National Research Council of Canada
Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon,
Saskatchewan, S7N 0W9, Canada
Tel: 306 975 4164
Fax: 306 975 4839
Email: Ed.Tsang@nrc-cnrc.gc.ca
High quality sequence stop: 453.
FEATURES
source
1..453
/organism="Brassica napus"
/mol_type="mRNA"
/db_xref="taxon:3708"
/clone_lib="Brassica napus 3ETMS"
/Note="Vector: pDNR-LIB_CREATOR; Site_1: SfiIA; Site_2:
SfiIB; Sequences have been trimmed to remove vector and
low quality regions using LUCY sequence cleanup software
(www.tigr.org)."

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# ORIGIN

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Alignment Scores:
Pred. No.:          1.86e-41          Length:          453
Score:             436.00             Matches:          79
Percent Similarity: 98.8%             Conservative:    0
Best Local Similarity: 98.8%           Mismatches:      1
Query Match:       98.6%               Indels:         0
DB:                6                  Gaps:           0

US-09-759-584-49 (1-80) x CD834008 (1-453)

QY  1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  51 ATGGCTAAGTTTGCTTCCATCATTCGCCCTACTTTTGGCTGCTCTTGTCTCTTTCGCTGCT 110

QY  21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTTP 40
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  111 CTCGAAGCACCACCAATGTTGGAAGCACAGAAGTTGTGCGAGAGGCCAAGTGGGACATGG 170
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QY  41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  171 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGATCAGTCATTAACCTTGAGAAGCA 230

QY  61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  231 CGACATGGATCTTGCAACTATGTCTTCCAGCTCACAAAGTGTATTGTCTACTTCCCTTGT 290

RESULT 12
CN726424
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CN726424
3ETMS UP_003_H02_10JUN2003_001 Brassica napus 3ETMS Brassica napus
cDNA 5', mRNA sequence.
CN726424
CN726424.1 GI:65284226
EST.
Brassica napus (rape)
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 453)

REFERENCE
Tsang,E.
Gene expression in seed germination in Brassica napus
Unpublished (2004)
Contact: Ed Tsang
Plant Natural Products
National Research Council of Canada
Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon,
Saskatchewan, S7N 0W9, Canada
Tel: 306 975 4164
Fax: 306 975 4839
Email: Ed.Tsang@nrc-cnrc.gc.ca
High quality sequence stop: 453.
FEATURES
source
1..453
/organism="Brassica napus"
/mol_type="mRNA"
/db_xref="taxon:3708"
/clone_lib="Brassica napus 3ETMS"
/Note="Vector: pDNR-LIB_CREATOR; Site_1: SfiIA; Site_2:
SfiIB; Sequences have been trimmed to remove vector and
low quality regions using LUCY sequence cleanup software
(www.tigr.org)."

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# ORIGIN

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Alignment Scores:
Pred. No.:          1.86e-41          Length:          453
Score:             436.00             Matches:          79
Percent Similarity: 98.8%             Conservative:    0
Best Local Similarity: 98.8%           Mismatches:      1
Query Match:       98.6%               Indels:         0
DB:                7                  Gaps:           0

US-09-759-584-49 (1-80) x CN726424 (1-453)

QY  1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  51 ATGGCTAAGTTTGCTTCCATCATTCGCCCTACTTTTGGCTGCTCTTGTCTCTTTCGCTGCT 110

QY  21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTTP 40
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  111 CTCGAAGCACCACCAATGTTGGAAGCACAGAAGTTGTGCGAGAGGCCAAGTGGGACATGG 170

QY  41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  171 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGATCAGTCATTAACCTTGAGAAGCA 230

QY  61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  231 CGACATGGATCTTGCAACTATGTCTTCCAGCTCACAAAGTGTATTGTCTACTTCCCTTGT 290
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RESULT 13
CN726661
LOCUS
DEFINITION
3ETMS UP 006_G02_10JUN2003_002 Brassica napus 3ETMS Brassica napus
cDNA 5', mRNA sequence.
ACCESSION
CN726661
VERSION
CN726661.1 GI:65284463
KEYWORDS
EST.
SOURCE
Brassica napus (rape)
ORGANISM
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 456)
Tsang, E.
Gene expression in seed germination in Brassica napus
Unpublished (2004)
CONTACT
Ed Tsang
Plant Natural Products
National Research Council of Canada
Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon,
Saskatchewan, S7N 0W9, Canada
Tel: 306 975 4164
Fax: 306 975 4839
Email: Ed.Tsang@nrc-cnrc.gc.ca
High quality sequence stop: 456.
FEATURES
source
1..456
Location/Qualifiers
/organism="Brassica napus"
/mol_type="mRNA"
/db_xref="taxon:3708"
/clone_lib="Brassica napus 3ETMS"
/note="Vector: pDNR-LIB CREATOR; Site 1: SfiIA; Site 2:
SfiIB; Sequences have been trimmed to remove vector and
low quality regions using LUCY sequence cleanup software
(www.tigr.org)."
ORIGIN
Alignment Scores:
Pred. No.: 1..87e-41 Length: 456
Score: 436.00 Matches: 79
Percent Similarity: 98.8% Conservative: 0
Best Local Similarity: 98.8% Mismatches: 1
Query Match: 98.6% Indels: 0
DB: 7 Gaps: 0
US-09-759-584-49 (1-80) x CN726661 (1-456)
QY 1 MetAlaLysPheAlaSerIleAlaLeuPheAlaLeuValLeuPheAlaLa 20
Db 51 ATGGCTAAGTTTGGCTTCCATCATTTGCTGCTTTTGGCTGCTTTTGGCTGCT 110
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTTP 40
Db 111 CTCGAGACCAACCAATGTTGGAAGCAGCAAGATTGTGCGAGAGCCAAAGTGGACATGG 170
QY 41 SerGlyValCysGlyValAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
Db 171 TCAGGAGTCTGTGGAAACCAATACCGATCGCAAGATCAGTGCATTAACCTTGAGAAAGCA 230
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
Db 231 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAAGTGTATTGCTTACTTCCCTTGT 290
RESULT 14
CD828332
LOCUS
DEFINITION
BN25.070H07F020125 BN25 Brassica napus cDNA clone BN25070H07, mRNA
sequence.
ACCESSION
CD828332
VERSION
CD828332.1 GI:32510272
KEYWORDS
EST.
SOURCE
Brassica napus (rape)
ORGANISM
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 553)
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
CONTACT
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
FEATURES
source
1..480
Location/Qualifiers
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet Neuf"
/db_xref="taxon:3708"
/clone="BN25070H07"
/tissue_type="seed"
/clone_lib="BN25"
ORIGIN
Alignment Scores:
Pred. No.: 2e-41 Length: 480
Score: 436.00 Matches: 79
Percent Similarity: 98.8% Conservative: 0
Best Local Similarity: 98.8% Mismatches: 1
Query Match: 98.6% Indels: 0
DB: 6 Gaps: 0
US-09-759-584-49 (1-80) x CD828332 (1-480)
QY 1 MetAlaLysPheAlaSerIleAlaLeuPheAlaLeuValLeuPheAlaLa 20
Db 41 ATGGCTAAGTTTGGCTTCCATCATTTGCTGCTTTTGGCTGCTTTTGGCTGCT 100
QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTTP 40
Db 101 CTCGAGACCAACCAATGTTGGAAGCAGCAAGATTGTGCGAGAGCCAAAGTGGACATGG 160
QY 41 SerGlyValCysGlyValAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
Db 161 TCAGGAGTCTGTGGAAACCAATACCGATCGCAAGATCAGTGCATTAACCTTGAGAAAGCA 220
QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
Db 221 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAAGTGTATTGCTTACTTCCCTTGT 280
RESULT 15
CD831014
LOCUS
DEFINITION
BN40.047K12F011228 BN40 Brassica napus cDNA clone BN40047K12, mRNA
sequence.
ACCESSION
CD831014
VERSION
CD831014.1 GI:32512954
KEYWORDS
EST.
SOURCE
Brassica napus (rape)
ORGANISM
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 553)
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
CONTACT
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France

```

Tel: 33 1 69 47 54 00  
 Fax: 33 1 69 47 54 10  
 This sequence has been generated in the framework of the french  
 plant genomics programme 'Genoplante' (<http://www.genoplante.com>)  
 and <http://genoplante-info.inbio.gen.fr>.

FEATURES

source  
 1. .553  
 /organism="Brassica napus"  
 /mol\_type="mRNA"  
 /cultivar="Jet Neuf"  
 /db\_xref="taxon:3708"  
 /clone="BN40047K12"  
 /tissue type="seed"  
 /clone\_lib="BN40"

ORIGIN

Alignment Scores:  
 Pred. No.: 2.4e-41 Length: 553  
 Score: 436.00 Matches: 79  
 Percent Similarity: 98.8% Conservative: 0  
 Best Local Similarity: 98.8% Mismatches: 1  
 Query Match: 98.6% Indels: 0  
 DB: 6 Gaps: 0

US-09-759-584-49 (1-80) x CD831014 (1-553)

QY 1 MetAlaIySPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValIeuPheAlaAla 20  
 |||||  
 Db 50 ATGGCTAAGTTTGTCTTCCATCATTCCTTTTGTCTCTTCTTCTCTTCTTCTCTTCT 109  
 QY 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40  
 |||||  
 Db 110 CTCGAAGCCACCAACATGTGGAGGACACAGAGTTGTGGAGAGGCCAAGTGGACATGG 169  
 QY 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60  
 |||||  
 Db 170 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGATCAGTGCATTAACTTGAGAAAGCA 229  
 QY 61 ArgHisGlySerCysAsnTyrValPheProAlaHisIleCysIleCysTyrPheProCys 80  
 |||||  
 Db 230 CGACATGGATCTTGGCAACTATGTCTTCCAGCTCACAGGTGATTGTCTACTTCCCTTGT 289

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 Job time : 3004.5 secs